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12AP1/E5 -- Viventia Biotech	AI-201 -- AutoImmune
1964 -- Aventis	AI-301 -- AutoImmune
20K growth hormone -- AMUR	AIDS vaccine -- ANRS, CIBG, Hesed
28P6/E6 -- Viventia Biotech	Biomed, Hollis-Eden, Rome, United
3-Hydroxyphthaloyl-beta-lactoglobulin --	Biomedical, American Home Products,
4-IBB ligand gene therapy --	Maxygen
64-Cu MAb conjugate TETA-1A3 --	airway receptor ligand -- IC Innovations
Mallinckrodt Institute of Radiology	- AJvW 2 -- Ajinomoto
64-Cu MAb conjugate TETA-CT84.66	AK 30 NGF -- Alkermes
64-Cu Trastuzumab TETA conjugate --	Albuferon -- Human Genome Sciences
Genentech	albumin -- Biogen, DSM Anti-Infectives,
A 200 -- Amgen	Genzyme Transgenics, PPL Therapeutics,
A10255 -- Eli Lilly	TranXenoGen, Welfide Corp.
A1PDX -- Hedral Therapeutics	aldesleukin -- Chiron
A6 -- Angstrom	alefacept -- Biogen
aaAT-III -- Genzyme	Alemtuzumab --
Abciximab -- Centocor	Allergy therapy -- ALK-Abello/Maxygen,
ABI.001 -- Atlantic BioPharmaceuticals	ALK-Abello/RP Scherer
ABT-828 -- Abbott	allergy vaccines -- Allergy Therapeutics
Accutin	Alnidofibatide -- Aventis Pasteur
Actinohivin	Alnorine -- SRC VB VECTOR
activin -- Biotech Australia, Human	ALP 242 -- Gruenenthal
Therapeutics	Alpha antitrypsin -- Arriva/Hyland
activin -- Curis	Immuno/ProMetic/Protease Sciences
AD 439 -- Tanox	Alpha-1 antitrypsin -- Cutter, Bayer, PPL
AD 519 -- Tanox	Therapeutics, Profile, ZymoGenetics,
Adalimumab -- Cambridge Antibody Tech.	Arriva
Adenocarcinoma vaccine -- Biomira -- NIS	Alpha-1 protease inhibitor -- Genzyme
Adenosine A2B receptor antagonists --	Transgenics, Welfide Corp.
Adenosine Therapeutics	Alpha-galactose fusion protein --
ADP-001 -- Axis Genetics	Immunomedics
AF 13948 -- Affymax	Alpha-galactosidase A -- Research
Afelimomab -- Knoll	Corporation Technologies
AFP-SCAN -- Immunomedics	Alpha-glucosidase -- Genzyme, Novazyme
AG 2195 -- Corixa	Alpha-lactalbumin
agalsidase alfa -- Transkaryotic Therapies	Alpha-L-iduronidase -- Transkaryotic
agalsidase beta -- Genzyme	Therapies, BioMarin
AGENT-- Antisoma	alteplase -- Genentech
AI 300 -- AutoImmune	alvircept sudotox -- NIH
AI-101 -- Teva	ALX1-11 --sNPS Pharmaceuticals
AI-102 -- Teva	Alzheimer's disease gene therapy --

FIG. 1A

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AM-133 -- AMRAD	Anti-B4 MAb-DC1 conjugate -- ImmunoGen
Amb a 1 immunostim conj. -- Dynavax	Anti-B7 antibody PRIMATIZED -- IDEC
AMD 3100 -- AnorMED -- NIS	Anti-B7-1 MAb 16-10A1
AMD 3465 -- AnorMED -- NIS	Anti-B7-1 MAb 1G10
AMD 3465 -- AnorMED -- NIS	Anti-B7-2 MAb GL-1
AMD Fab -- Genentech	Anti-B7-2-gelonin immunotoxin --
Amediplase -- Menarini, Novartis	Antibacterials/antifungals --
AM-F9	Diversa/IntraBiotics
Amoebiasis vaccine	Anti-beta-amyloid monoclonal antibodies --
Amphiregulin -- Octagene	Cambridge Antibody Tech., Wyeth-Ayerst
anakinra -- Amgen	Anti-BLyS antibodies -- Cambridge
analgesic -- Nobex	Antibody Tech. /Human Genome Sciences
ancestim -- Amgen	Antibody-drug conjugates -- Seattle
AnergiX.RA -- Corixa, Organon	Genetics/Eos
Angiocidin -- InKine	Anti-C5 MAb BB5-1 -- Alexion
angiogenesis inhibitors -- ILEX	Anti-C5 MAb N19-8 -- Alexion
AngioMab -- Antisoma	Anti-C8 MAb
Angiopoietins -- Regeneron/Procter &	anticancer cytokines -- BioPulse
Gamble	anticancer matrix -- Telios Integra
angiostatin -- EntreMed	Anticancer monoclonal antibodies -- ARIUS,
Angiostatin/endostatin gene therapy --	Immunex
Genetix Pharmaceuticals	anticancer peptides -- Maxygen, Micrologix
angiotensin-II, topical -- Maret	Anticancer prodrug Tech. -- Alexion
Anthrax -- EluSys Therapeutics/US Army	Antibody Technologies
Medical Research Institute	anticancer Troy-Bodies -- Affite -- Affitech
Anthrax vaccine	anticancer vaccine -- NIH
Anti platelet-derived growth factor D human	anticancers -- Epimmune
monoclonal antibodies -- CuraGen	Anti-CCR5/CXCR4 sheep MAb -- KS
Anti-17-1A MAb 3622W94 --	Biomedix Holdings
GlaxoSmithKline	Anti-CD11a MAb KBA --
Anti-2C4 MAb -- Genentech	Anti-CD11a MAb M17
anti-4-1BB monoclonal antibodies -- Bristol-	Anti-CD11a MAb TA-3 --
Myers Squibb	Anti-CD11a MAb WT.1 --
Anti-Adhesion Platform Tech. -- Cytovax	Anti-CD11b MAb -- Pharmacia
Anti-adipocyte MAb -- Cambridge Antibody	Anti-CD11b MAb LM2
Tech./ObeSys	Anti-CD154 MAb -- Biogen
antiallergics -- Maxygen	Anti-CD16-anti-CD30 MAb -- Biotest
antiallergy vaccine -- Acambis	Anti-CD18 MAb -- Pharmacia
Anti-alpha-4-integrin MAb	Anti-CD19 MAb B43 --
Anti-angiogenesis monoclonal antibodies --	Anti-CD19 MAb -liposomal sodium butyrate
KS Biomedix/Schering AG	conjugate --

FIG. 1B

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Anti-CD19 MAb-saporin conjugate –	Anti-CD4 MAb KT6
Anti-CD19-dsFv-PE38-immunotoxin –	Anti-CD4 MAb OX38
Anti-CD2 MAb 12-15 –	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb B-E2 -- Diaclone	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX34 –	Anti-CD4 MAb W3/25
Anti-CD2 MAb OX54 –	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb OX55 –	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-1	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD2 MAb RM2-2	Anti-CD40 MAb
Anti-CD2 MAb RM2-4	Anti-CD40 MAb 5D12 – Tanox
Anti-CD20 MAb BCA B20	Anti-CD44 MAb A3D8
Anti-CD20-anti-Fc alpha RI bispecific MAb – Medarex, Tenovus	Anti-CD44 MAb GKWA3
Anti-CD22 MAb-saporin-6 complex –	Anti-CD44 MAb IM7
Anti-CD3 immunotoxin –	Anti-CD44 MAb KM81
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb humanised – Protein Design, RW Johnson	Anti-CD45RB MAb
Anti-CD3 MAb WT32	Anti-CD48 MAb HuLy-m3
Anti-CD3 MAb-ricin-chain-A conjugate –	Anti-CD48 MAb WM-63
Anti-CD3 MAb-xanthine-oxidase conjugate –	Anti-CD5 MAb -- Becton Dickinson
–	Anti-CD5 MAb OX19
Anti-CD30 MAb BerH2 -- Medac	Anti-CD6 MAb
Anti-CD30 MAb-saporin conjugate	Anti-CD7 MAb-PAP conjugate
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD38 MAb AT13/5	Anti-CD8 MAb – Amerimmune, Cytodyn, Becton Dickinson
Anti-CD38 MAb-saporin conjugate	Anti-CD8 MAb 2-43
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD8 MAb OX8
Anti-CD3-anti-EGFR MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD80 MAb P7C10 -- ID Vaccine
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD8-idarubicin conjugate
Anti-CD3-anti-SCLC bispecific MAb	Anti-CEA MAb CE-25
Anti-CD4 idiotype vaccine	Anti-CEA MAb MN 14 – Immunomedics
Anti-CD4 MAb – Centocor, IDEC Pharmaceuticals, Xenova Group	Anti-CEA MAb MN14-PE40 conjugate – Immunomedics
Anti-CD4 MAb 16H5	Anti-CEA MAb T84.66-interleukin-2 conjugate
Anti-CD4 MAb 4162W94 -- GlaxoSmithKline	Anti-CEA sheep MAb -- KS Biomedix Holdings
Anti-CD4 MAb B-F5 -- Diaclone	
Anti-CD4 MAb GK1-5	

FIG. 1C

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Anti-cell surface monoclonal antibodies --	Anti-HIV antibody -- Epicyte
Cambridge Antibody Tech. /Pharmacia	anti-HIV catalytic antibody -- Hesed Biomed
Anti-c-erbB2-anti-CD3 bifunctional MAb --	anti-HIV fusion protein -- Idun
Otsuka	anti-HIV proteins -- Cangene
Anti-CMV MAb -- Scotgen	Anti-HM1-24 MAb -- Chugai
Anti-CTLA-4 MAb	Anti-hR3 MAb
Anti-EGFR catalytic antibody -- Hesed	Anti-Human-Carcinoma-Antigen MAb --
Biomed	Epicyte
anti-EGFR immunotoxin -- IVAX	Anti-ICAM-1 MAb -- Boehringer Ingelheim
Anti-EGFR MAb -- Abgenix	Anti-ICAM-1 MAb 1A-29 -- Pharmacia
Anti-EGFR MAb 528	Anti-ICAM-1 MAb HA58
Anti-EGFR MAb KSB 107 -- KS Biomedix	Anti-ICAM-1 MAb YN1/1.7.4
Anti-EGFR MAb-DM1 conjugate --	Anti-ICAM-3 MAb ICM3 -- ICOS
ImmunoGen	Anti-idiotypic breast cancer vaccine 11D10
Anti-EGFR MAb-LA1 --	Anti-idiotypic breast cancer vaccine
Anti-EGFR sheep MAb -- KS Biomedix	ACA14C5 --
Anti-FAP MAb F19-I-131	Anti-idiotypic cancer vaccine -- ImClone
Anti-Fas IgM MAb CH11	Systems/Merck KGaA ImClone, Viventia
Anti-Fas MAb Jo2	Biotech
Anti-Fas MAb RK-8	Anti-idiotypic cancer vaccine 1A7 -- Titan
Anti-Flt-1 monoclonal antibodies -- ImClone	Anti-idiotypic cancer vaccine 3H1 -- Titan
Anti-fungal peptides -- State University of	Anti-idiotypic cancer vaccine TriAb -- Titan
New York	Anti-idiotypic Chlamydia trachomatis
antifungal tripeptides -- BTG	vaccine
Anti-ganglioside GD2 antibody-interleukin-2	Anti-idiotypic colorectal cancer vaccine --
fusion protein -- Lexigen	Novartis
Anti-GM2 MAb -- Kyowa	Anti-idiotypic colorectal cancer vaccine --
Anti-GM-CSF receptor monoclonal	Onyvax
antibodies -- AMRAD	Anti-idiotypic melanoma vaccine -- IDEC
Anti-gp130 MAb -- Tosoh	Pharmaceuticals
Anti-HCA monoclonal antibodies --	Anti-idiotypic ovarian cancer vaccine ACA
AltaRex/Epigen	125
Anti-hCG antibodies -- Abgenix/AVI	Anti-idiotypic ovarian cancer vaccine AR54 -
BioPharma	- AltaRex
Anti-heparanase human monoclonal	Anti-idiotypic ovarian cancer vaccine CA-
antibodies -- Oxford	125 -- AltaRex, Biomira
Glycosciences/Medarex	Anti-IgE catalytic antibody -- Hesed Biomed
Anti-hepatitis C virus human monoclonal	Anti-IgE MAb E26 -- Genentech
antibodies -- XTL Biopharmaceuticals	Anti-IGF-1 MAb
Anti-HER-2 antibody gene therapy	anti-inflammatory -- GeneMax
Anti-herpes antibody -- Epicyte	anti-inflammatory peptide -- BTG

FIG. 1D

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anti-integrin peptides -- Burnha	Anti-mu MAb -- Novartis
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC-1 MAb
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody - - Advanced Biotherapy	Anti-nuclear autoantibodies -- Procyon
Anti-interleukin-10 MAb --	Anti-ovarian cancer monoclonal antibodies -
Anti-interleukin-12 MAb --	- Dompe
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Anti-p185 monoclonal antibodies
Anti-interleukin-2 receptor MAb 2A3	Anti-p43 MAb
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb ART-18	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-2 receptor MAb NDS61	Anti-Rev MAb gene therapy --
Anti-interleukin-4 MAb 11B11	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-6 MAb -- Centocor, Diaclone, Pharmadigm	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-8 MAb -- Xenotech	Anti-RT gene therapy
Anti-JL1 MAb	Antisense K-ras RNA gene therapy
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-SF-25 MAb
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-sperm antibody -- Epicyte
Anti-LCG MAb -- Cytoclinal	Anti-Tac(Fv)-PE38 conjugate
Anti-lipopolysaccharide MAb -- VitaResc	Anti-TAPA/CD81 MAb AMP1
Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University	Anti-tat gene therapy
Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital	Anti-TCR-alphabeta MAb H57-597
Anti-MHC monoclonal antibodies	Anti-TCR-alphabeta MAb R73
Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences	Anti-tenascin MAb BC-4-I-131
Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings	Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme
	Anti-TGF-beta MAb 2G7 -- Genentech
	Antithrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad
	Anti-Thy1 MAb
	Anti-Thy1.1 MAb

FIG. 1E

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Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix	ARGENT gene delivery systems -- ARIAD
Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono	Arresten
Anti-TNF sheep MAb -- KS Biomedix Holdings	ART-123 -- Asahi Kasei
Anti-TNFalpha MAb -- Genzyme	arylsulfatase B -- BioMarin
Anti-TNFalpha MAb B-C7 -- Diaclone	Arylsulfatase B, Recombinant human -- BioMarin
Anti-tooth decay MAb -- Planet BioTech.	AS 1051 -- Ajinomoto
antitumour RNases -- NIH	ASI-BCL -- Intracell
Anti-VCAM MAb 2A2 -- Alexion	ATL-101 -- Alizyme
Anti-VCAM MAb 3F4 -- Alexion	atrial natriuretic peptide -- Pharis
Anti-VCAM-1 MAb	Aurintricarboxylic acid-high molecular weight
Anti-VEC MAb -- ImClone	autoimmune disorders -- GPC Biotech/MorphoSys
Anti-VEGF MAb -- Genentech	Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme
Anti-VEGF MAb 2C3	Tra
Anti-VEGF sheep MAb -- KS Biomedix Holdings	Autoimmune disorders/cancer -- Abgenix/Chiron, /CuraGen
Anti-VLA-4 MAb HP1/2 -- Biogen	Autotaxin
Anti-VLA-4 MAb PS/2	Avicidin -- NeoRx
Anti-VLA-4 MAb R1-2	axogenesis factor-1 -- Boston Life Sciences
Anti-VLA-4 MAb TA-2	Axokine -- Regeneron
Anti-VRE sheep MAb -- KS Biomedix Holdings	B cell lymphoma vaccine -- Biomira
ANUP -- TranXenoGen	B7-1 gene therapy --
ANUP-1 -- Pharis	BABS proteins -- Chiron
AOP-RANTES -- Senetek	BAM-002 -- Novelos Therapeutics
Apan-CH -- Praecis Pharmaceuticals	Bay-16-9996 -- Bayer
APC-8024 -- Demegen	Bay-39-9437 -- Bayer
ApoA-1 -- Milano, Pharmacia	Bay-50-4798 -- Bayer
Apogen -- Alexion	BB-10153 -- British Biotech
apolipoprotein A1 -- Avanir	BBT-001 -- Bolder BioTech.
Apolipoprotein E -- Bio-Tech. General	BBT-002 -- Bolder BioTech.
Applaggin -- Biogen	BBT-003 -- Bolder BioTech.
aprotinin -- ProdiGene	BBT-004 -- Bolder BioTech.
APT-070C -- AdProTech	BBT-005 -- Bolder BioTech.
AR 177 -- Aronex Pharmaceuticals	BBT-006 -- Bolder BioTech.
AR 209 -- Aronex Pharmaceuticals, Antigenics	BBT-007 -- Bolder BioTech.
AR545C	BCH-2763 -- Shire
	BCSF -- Millenium Biologix
	BDNF -- Regeneron -- Amgen

FIG. 1F

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Becaplermin -- Johnson & Johnson, Chiron	BST-3002 -- BioStratum
Bectumomab -- Immunomedics	BTI 322 --
Beta-adrenergic receptor gene therapy -- University of Arkansas	butyrylcholinesterase -- Shire
BI 51013 -- Behringwerke AG	C 6822 -- COR Therapeutics
BIBH 1 -- Boehringer Ingelheim	C1 esterase inhibitor -- Pharming
BIM-23190 -- Beaufour-Ipsen	C3d adjuvant -- AdProTech
birch pollen immunotherapy -- Pharmacia	CAB-2.1 -- Millennium
bispecific fusion proteins -- NIH	calcitonin -- Inhale Therapeutics Systems, Aventis, Genetronics, TranXenoGen, Unigene, Rhone Poulenc Rohrer
Bispecific MAb 2B1 -- Chiron	calcitonin -- oral -- Nobex, Emisphere, Pharmaceutical Discovery
Bitistatin	Calcitonin gene-related peptide -- Asahi Kasei -- Unigene
BIWA 4 -- Boehringer Ingelheim	calcitonin, human -- Suntory
blood substitute -- Northfield, Baxter Intl.	calcitonin, nasal -- Novartis, Unigene
BLP-25 -- Biomira	calcitonin, Panoderm -- Elan
BLS-0597 -- Boston Life Sciences	calcitonin, Peptitrol -- Shire
BLYS -- Human Genome Sciences	calcitonin, salmon -- Therapicon
BLYS radiolabelled -- Human Genome Sciences	calin -- Biopharm
BM 06021 -- Boehringer Mannheim	Calphobindin I
BM-202 -- BioMarin	calphobindin I -- Kowa
BM-301 -- BioMarin	calreticulin -- NYU
BM-301 -- BioMarin	Campath-1G
BM-302 -- BioMarin	Campath-1M
BMP 2 -- Genetics Institute/Medtronic- Sofamor Danek, Genetics Institute/ Collagenesis, Genetics Institute/Yamanouch	cancer therapy -- Cangene
BMP 2 gene therapy	cancer vaccine -- Aixlie, Aventis Pasteur, Center of Molecular Immunology, YM BioSciences, Cytos, Genzyme, Transgenics, GlobelImmune, Igeneon, ImClone, Virogenetics, InterCell, Iomai, Jenner Biotherapies, Memorial Sloan- Kettering Cancer Center, Sydney Kimmel Cancer Center, Novavax, Protein Sciences, Argonex, SIGA
BMP 52 -- Aventis Pasteur, Biopharm	Cancer vaccine ALVAC-CEA B7.1 -- Aventis Pasteur/Therion Biologics
BMP-2 -- Genetics Institute	Cancer vaccine CEA-TRICOM -- Aventis Pasteur/Therion Biologics
BMS 182248 -- Bristol-Myers Squibb	Cancer vaccine gene therapy -- Cantab Pharmaceuticals
BMS 202448 -- Bristol-Myers Squibb	
bone growth factors -- IsoTis	
BPC-15 -- Pfizer	
brain natriuretic peptide --	
Breast cancer -- Oxford GlycoSciences/Medarex	
Breast cancer vaccine -- Therion Biologics, Oregon	
BSSL -- PPL Therapeutics	
BST-2001 -- BioStratum	

FIG. 1G

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Cancer vaccine HER-2/neu -- Corixa	CETP vaccine -- Avant
Cancer vaccine THERATOPE -- Biomira	Cetrorelix
cancer vaccine, PolyMASC -- Valentis	Cetuximab
Candida vaccine -- Corixa, Inhibitex	CGH 400 -- Novartis
Canstatin -- ILEX	CGP 42934 -- Novartis
CAP-18 -- Panorama	CGP 51901 -- Tanox
Cardiovascular gene therapy -- Collateral Therapeutics	CGRP -- Unigene
carperitide -- Suntory	CGS 27913 -- Novartis
Casocidin-1 -- Pharis	CGS 32359 -- Novartis
CAT 152 -- Cambridge Antibody Tech.	Chagas disease vaccine -- Corixa
CAT 192 -- Cambridge Antibody Tech.	chemokines -- Immune Response
CAT 213 -- Cambridge Antibody Tech.	CHH 380 -- Novartis
Catalase -- Enzon	chitinase -- Genzyme, ICOS
Cat-PAD -- Circassia	Chlamydia pneumoniae vaccine -- Antex Biologics
CB 0006 -- Celltech	Chlamydia trachomatis vaccine -- Antex Biologics
CCK(27-32) -- Akzo Nobel	Chlamydia vaccine -- GlaxoSmithKline
CCR2-64I -- NIH	Cholera vaccine CVD 103-HgR -- Swiss Serum and Vaccine Institute Berne
CD, Procept -- Paligent	Cholera vaccine CVD 112 -- Swiss Serum and Vaccine Institute Berne
CD154 gene therapy	Cholera vaccine inactivated oral -- SBL Vaccin
CD39 -- Immunex	Chrysalin -- Chrysalis BioTech.
CD39-L2 -- Hyseq	CI-782 -- Hitachi Kase
CD39-L4 -- Hyseq	Ciliary neurotrophic factor -- Fidia, Roche
CD4 fusion toxin -- Senetek	CIM project -- Active Biotech
CD4 IgG -- Genentech	CL 329753 -- Wyeth-Ayerst
CD4 receptor antagonists -- Pharmacopeia/Progenics	CL22, Cobra -- ML Laboratories
CD4 soluble -- Progenics	Clenoliximab -- IDEC
CD4, soluble -- Genzyme Transgenics	Clostridium difficile antibodies -- Epicyte
CD40 ligand -- Immunex	clotting factors -- Octogene
CD4-ricin chain A -- Genentech	CMB 401 -- Celltech
CD59 gene therapy -- Alexion	CNTF -- Sigma-Tau
CD8 TIL cell therapy -- Aventis Pasteur	Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps
CD8, soluble -- Avidex	coccidiomycosis vaccine -- Arizo
CD95 ligand -- Roche	collagen -- Type I -- Pharming
CDP 571 -- Celltech	Collagen formation inhibitors -- FibroGen
CDP 850 -- Celltech	
CDP 870 -- Celltech	
CDS-1 -- Ernest Orlando	
Cedelizumab -- Ortho-McNeil	
Cetermin -- Insmmed	

FIG. 1H

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Collagen/hydroxyapatite/bone growth factor	CY 1747 -- Epimmune
-- Aventis Pasteur, Biopharm, Orquest	CY 1748 -- Epimmune
collagenase -- BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine -- Wistar Institute	Cystic fibrosis therapy -- CBR/IVAX
Component B, Recombinant -- Serono	CYT 351
Connective tissue growth factor inhibitors --	cytokine Traps -- Regeneron
FibroGen/Taisho	cytokines -- Enzon, Cytoclonal
Contortrostatin	Cytomegalovirus glycoprotein vaccine --
contraceptive vaccine -- Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible --	Cytomegalovirus vaccine live -- Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida --	Cytosine deaminase gene therapy --
Zonagen	GlaxoSmithKline
Copper-64 labelled MAb TETA-1A3 -- NCI	DA-3003 -- Dong-A
Coralyne	DAB389interleukin-6 -- Senetek
Corsevin M	DAB389interleukin-7
C-peptide analogues -- Schwarz	DAMP ^Δ -- Incyte Genomics
CPI-1500 -- Consensus	Daniplestim -- Pharmacia
CRF -- Neurobiological Tech.	darbepoetin alfa -- Amgen
cRGDfV pentapeptide --	DBI-3019 -- Diabetogen
CRL 1095 -- CytRx	DCC -- Genzyme
CRL 1336 -- CytRx	DDF -- Hyseq
CRL 1605 -- CytRx	decorin -- Integra, Telios
CS-560 -- Sankyo	defensins -- Large Scale Biology
CSF -- ZymoGenetics	DEGR-VIIa
CSF-G -- Hangzhou, Dong-A, Hanmi	Deimmunised antibody 3B6/22 AGEN
CSF-GM -- Cangene, Hunan, LG Chem	Deimmunised anti-cancer antibodies --
CSF-M -- Zarix	Biovation/Viragen
CT 1579 -- Merck Frosst	Dendroamide A
CT 1786 -- Merck Frosst	Dengue vaccine -- Bavarian Nordic, Merck
CT-112 ^Δ -- BTG	denileukin difitox -- Ligand
CTB-134L -- Xenova	DES-1101 -- Desmos
CTC-111 -- Kaketsuken	desirudin -- Novartis
CTGF -- FibroGen	desmopressin -- Unigene
CTLA4-Ig -- Bristol-Myers Squibb	Desmoteplase -- Merck, Schering AG
CTLA4-Ig gene therapy --	Destabilase
CTP-37 -- AVI BioPharma	Diabetes gene therapy -- DeveloGen, Pfizer
C-type natriuretic peptide -- Suntory	Diabetes therapy -- Crucell
CVS 995 -- Corvas Intl.	Diabetes type 1 vaccine -- Diamyd
CX 397 -- Nikko Kyodo	Therapeutics

FIG. 11

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DiaCIM -- YM BioSciences	EGF-P64k vaccine -- Center of Molecular Immunology
dialytic oligopeptides -- Research Corp	EL 246 -- LigoCyte
Diamyd -- Diamyd Therapeutics	elastase inhibitor -- Synergen
DiaPep227-- Pepgen	elcatonin -- Therapicon
DiavaX -- Corixa	EMD 72000 -- Merck KGaA
Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline	Emdogain -- BIORA
DIR therapy -- Solis Therapeutics --	emfilermin -- AMRAD
DNase -- Genentech	Emoctakin -- Novartis
Dornase alfa -- Genentech	enamel matrix protein -- BIORA
Dornase alfa, inhalation -- Genentech	Endo III -- NYU
Doxorubicin-anti-CEA MAb conjugate -- Immunomedics	endostatin -- EntreMed, Pharis
DP-107 -- Trimeris	Enhancins -- Micrologix
drotrecogin alfa -- Eli Lilly	Enlimomab -- Isis Pharm.
DTctGMCSF	Enoxaparin sodium -- Pharmuka
DTP-polio vaccine -- Aventis Pasteur	enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings
DU 257-KM231 antibody conjugate -- Kyowa	Eosinophil-derived neutralizing agent --
dural graft matrix -- Integra	EP-51216 -- Asta Medica
Dutepase -- Baxter Intl.	EP-51389 -- Asta Medica
DWP-401 -- Daewoong	EPH family ligands -- Regeneron
DWP-404 -- Daewoong	Epidermal growth factor -- Hitachi Kasei, Johnson & Johnson
DWP-408 -- Daewoong	Epidermal growth factor fusion toxin -- Senetek
E coli O157 vaccine -- NIH	Epidermal growth factor-genistein --
E21-R -- BresaGen	EPI-HNE-4 -- Dyax
Eastern equine encephalitis virus vaccine --	EPI-KAL2 -- Dyax
Echicetin --	Epoetin-alfa -- Amgen, Dragon Pharmaceuticals, Nanjing Huaxin
Echinhibin 1 --	Epratuzumab -- Immunomedics
Echistatin -- Merck	Epstein-Barr virus vaccine --
Echitamine --	Aviron/SmithKline Beecham, Bioresearch
EC-SOD -- PPL Therapeutics	Eptacog alfa -- Novo Nordisk
EDF -- Ajinomoto	Eptifibatide -- COR Therapeutics
EDN derivative -- NIH	erb-38 --
EDNA -- NIH	Erlizumab -- Genentech
Edobacomab -- XOMA	
Edrecolomab -- Centocor	
EF 5077	
Efalizumab -- Genentech	
EGF fusion toxin -- Seragen, Ligand	

FIG. 1J

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erythropoietin -- Alkermes, ProLease, Dong-A, Elanex, Genetics Institute, LG Chem, Protein Sciences, Serono, Snow Brand, SRC VB VECTOR, Transkaryotic Therapies	Felvizumab -- Scotgen
Erythropoietin Beta -- Hoffman La Roche	FFR-VIIa -- Novo Nordisk
Erythropoietin/Epoetin alfa -- Chugai	FG-001 -- F-Gene
Escherichia coli vaccine -- North American Vaccine, SBL Vaccin, Swiss Serum and Vaccine Institute Berne	FG-002 -- F-Gene
etanercept -- Immunex	FG-004 -- F-Gene
examorelin -- Mediolanum	FG-005 -- F-Gene
exonuclease VII	FGF + fibrin -- Repair
F 105 -- Centocor	Fibrimage -- Bio-Tech. General
F-992 -- Fomix	fibrin-binding peptides -- ISIS Innovation
Factor IX -- Alpha Therapeutics, Wellfide Corp., CSL, enetics Institute/AHP, Pharmacia, PPL Therapeutics	fibrinogen -- PPL Therapeutics, Pharming
Factor IX gene therapy -- Cell Genesys	fibroblast growth factor -- Chiron, NYU, Ramot, ZymoGenetics
Factor VII -- Novo Nordisk, Bayer, Baxter Intl.	fibrolase conjugate -- Schering AG
Factor VIIa -- PPL Therapeutics, ZymoGenetics	Filgrastim -- Amgen
Factor VIII -- Bayer Genentech, Beaufour-Ipsen, CLB, Inex, Octagen, Pharmacia, Pharming	filgrastim -- PDA modified -- Xencor
Factor VIII -- PEGylated -- Bayer	FLT-3 ligand -- Immunex
Factor VIII fragments -- Pharmacia	FN18 CRM9 --
Factor VIII gene therapy -- Targeted Genetics	follicle-stimulating hormone -- Biotech Australia, Human Therapeutics
Factor VIII sucrose formulation -- Bayer, Genentech	follicle-stimulating hormone alfa -- Alkermes, ProLease, PowderJect, Serono, Akzo Nobel
Factor VIII-2 -- Bayer	Follicle-stimulating hormone Beta -- Bayer, Organon
Factor VIII-3 -- Bayer	FP 59
Factor Xa inhibitors -- Merck, Novo Nordisk, Mochida	FSH -- Ferring
Factor XIII -- ZymoGenetics	FSH + LH -- Ferring
Factors VIII and IX gene therapy -- Genetics Institute/Targeted Genetics	F-spondin -- CeNeS
Famoxin -- Genset	fusion protein delivery system -- UAB Research Foundation
Fas (delta) TM protein -- LXR BioTech.	fusion toxins -- Boston Life Sciences
	G 5598 -- Genentech
	GA-II -- Transkaryotic Therapies
	Gamma-interferon analogues -- SRC VB VECTOR
	Ganirelix -- Roche
	gastric lipase -- Meristem
	Gavilimomab --
	G-CSF -- Amgen, SRC VB VECTOR
	GDF-1 -- CeNeS
	GDF-5 -- Biopharm
	GDNF -- Amgen

FIG. 1K

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gelsolin -- Biogen	H5N1 influenza A virus vaccine -- Protein Sciences
Gemtuzumab ozogamicin -- Celltech	haemoglobin -- Biopure
Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies	haemoglobin 3011, Recombinant -- Baxter Healthcare
Glanzmann thrombasthenia gene therapy --	haemoglobin crosfumaril -- Baxter Intl.
Glatiramer acetate -- Yeda	haemoglobin stabilized -- Ajinomoto
glial growth factor 2 -- CeNeS	haemoglobin, recombinant -- Apex
GLP-1 -- Amylin, Suntory, TheraTech, Watson	HAF -- Immune Response
GLP-1 peptide analogues -- Zealand Pharmaceuticals	Hantavirus vaccine
glucagon -- Eli Lilly, ZymoGenetics	HB 19
Glucagon-like peptide-1 7-36 amide -- Suntory	HBNF -- Regeneron
Glucocerebrosidase -- Genzyme	HCC-1 -- Pharis
glutamate decarboxylase -- Genzyme Transgenics	hCG -- Milkhaus
Glycoprotein S3 -- Kureha	hCG vaccine -- Zonagen
GM-CSF -- Immunex	HE-317 -- Hollis-Eden Pharmaceuticals
GM-CSF tumour vaccine -- PowderJect	Heat shock protein cancer and influenza vaccines -- StressGen
GnRH immunotherapeutic -- Protherics	Helicobacter pylori vaccine -- Acambis, AstraZeneca/CSL, Chiron, Provalis
gp75 antigen -- ImClone	Helistat-G -- GalaGen
gp96 -- Antigenics	Hemolink -- Hemosol
GPI 0100 -- Galenica	hepapoietin -- Snow Brand
GR 4991W93 -- GlaxoSmithKline	heparanase -- InSight
Granulocyte colony-stimulating factor -- Dong-A	heparinase I -- Ibex
Granulocyte colony-stimulating factor conjugate	heparinase III -- Ibex
grass allergy therapy -- Dynavax	Hepatitis A vaccine -- American Biogenetic Sciences
GRF1-44 -- ICN	Hepatitis A vaccine inactivated
Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo	Hepatitis A vaccine Nothav -- Chiron
growth factor peptides -- Biotherapeutics	Hepatitis A-hepatitis B vaccine -- GlaxoSmithKline
growth hormone -- LG Chem	hepatitis B therapy -- Tripep
growth hormone, Recombinant human -- Sero	Hepatitis B vaccine -- Amgen, Chiron SpA, Meiji Milk, NIS, Prodeva, PowderJect, Rhein Biotech
GT 4086 -- Gliatech	Hepatitis B vaccine recombinant -- Evans Vaccines, Eptec Comblotech, Genentech, MedImmune, Merck Sharp & Dohme, Rhein Biotech, Shantha Biotechnics, Vector, Yeda
GW 353430 -- GlaxoSmithKline	
GW-278884 -- GlaxoSmithKline	
H 11 -- Viventia Biotech.	

FIG. 1L

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Hepatitis B vaccine recombinant TGP 943 -- Takeda	HIV peptides -- American Home Products
Hepatitis C vaccine -- Bavarian Nordic, Chiron, Innogenetics Acambis,	HIV vaccine -- Applied bioTech., Axis Genetics, Biogen, Bristol-Myers Squibb, Genentech, Korea Green Cross, NIS, Oncogen, Protein Sciences Corporation, Terumo, Tonen Corporation, Wyeth-Ayerst, Wyeth-Lederle Vaccines-Malvern, Advanced BioScience Laboratories, Bavarian Nordic, Bavarian Nordic/Statens Serum Institute, GeneCure, Immune Response, Progenics, Therion Biologics, United Biomedical, Chiron
Hepatitis D vaccine -- Chiron Vaccines	
Hepatitis E vaccine recombinant -- Genelabs/GlaxoSmithKline, Novavax	
hepatocyte growth factor -- Panorama, Sosei	
hepatocyte growth factor kringle fragments - - EntreMed	
Her-2/Neu peptides -- Corixa	
Herpes simplex glycoprotein DNA vaccine -- Merck, Wyeth-Lederle Vaccines-Malvern, Genentech, GlaxoSmithKline, Chiron, Takeda	HIV vaccine vCP1433 -- Aventis Pasteur
Herpes simplex vaccine -- Cantab Pharmaceuticals, CEL-SCI, Henderson Morley	HIV vaccine vCP1452 -- Aventis Pasteur
Herpes simplex vaccine live -- ImClone Systems/Wyeth-Lederle, Aventis Pasteur	HIV vaccine vCP205 -- Aventis Pasteur
HGF derivatives -- Dompe	HL-9 -- American BioScience
hIAPP vaccine -- Crucell	HM-9239 -- Cytran
Hib-hepatitis B vaccine -- Aventis Pasteur	HML-103 -- Hemosol
HIC 1	HML-104 -- Hemosol
HIP-- Altachem	HML-105 -- Hemosol
Hirudins -- Biopharma, Cangene, Dongkook, Japan Energy Corporation, Pharmacia Corporation, SIR International, Sanofi-Synthelabo, Sotragene, Rhein Biotech	HML-109 -- Hemosol
HIV edible vaccine -- ProdiGene	HML-110 -- Hemosol
HIV gp120 vaccine -- Chiron, Ajinomoto, GlaxoSmithKline, ID Vaccine, Progenics, VaxGen	HML-121 -- Hemosol
HIV gp120 vaccine gene therapy --	hNLP -- Pharis
HIV gp160 DNA vaccine -- PowderJect, Aventis Pasteur, Oncogen, Hyland Immuno, Protein Sciences	Hookworm vaccine
HIV gp41 vaccine -- Panacos	host-vector vaccines -- Henogen
HIV HGP-30W vaccine -- CEL-SCI	HPM 1 -- Chugai
HIV immune globulin -- Abbott, Chiron	HPV vaccine -- MediGene
	HSA -- Meristem
	HSF -- StressGen
	HSP carriers -- Weizmann, Yeda, Peptor
	HSPPC-70 -- Antigenics
	HSPPC-96 -- pathogen-derived -- Antigenics
	HSV 863 -- Novartis
	HTLV-I DNA vaccine
	HTLV-I vaccine
	HTLV-II vaccine -- Access
	HU 901 -- Tanox
	Hu23F2G -- ICOS
	HuHMFG1

FIG. 1M

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HumaLYM -- Intracell	HuMax-IL15 -- Genmab
Human krebs statika -- Yamanouchi	HYB 190 -- Hybridon
human monoclonal antibodies --	HYB 676 -- Hybridon
Abgenix/Biogen, Abgenix/ Corixa,	I-125 MAb A33 -- Celltech
Abgenix/Immunex, Abgenix/Lexicon,	Ibritumomab tiuxetan -- IDEC
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9401 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IBT-9402 -- Ibex
Centocor/Medarex, Corixa/Kirin Brewery,	IC 14 -- ICOS
Corixa/Medarex, Eos BioTech./Medarex,	Idarubicin anti-Ly-2.1 --
Eos/Xenerex, Exelixis/Protein Design	IDEC 114 -- IDEC
Labs, ImmunoGen/ Raven,	IDEC 131 -- IDEC
Medarex/B.Twelve,	IDEC 152 -- IDEC
MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals
Human monoclonal antibodies --	iduronate-2-sulfatase -- Transkaryotic
Medarex/Northwest Biotherapeutics,	Therapies
Medarex/Seattle Genetics	IGF/IBP-2-13 -- Pharis
human netrin-1 -- Exelixis	IGN-101 -- Igeneon
human papillomavirus antibodies -- Epicyte	IK HIR02 -- Iketon
Human papillomavirus vaccine -- Biotech	IL-11 -- Genetics Institute/AHP
Australia, IDEC, StressGen	IL-13-PE38 -- NeoPharm
Human papillomavirus vaccine MEDI 501 --	IL-17 receptor -- Immunex
MedImmune/GlaxoSmithKline	IL-18BP -- Yeda
Human papillomavirus vaccine MEDI	IL-1Hy1 -- Hyseq
503/MEDI 504 --	IL-1 β -- Celltech
MedImmune/GlaxoSmithKline	IL-1 β adjuvant -- Celltech
Human papillomavirus vaccine TA-CIN --	IL-2 -- Chiron
Cantab Pharmaceuticals	IL-2 + IL-12 -- Hoffman La-Roche
Human papillomavirus vaccine TA-HPV --	IL-6/sIL-6R fusion -- Hadasit
Cantab Pharmaceuticals	IL-6R derivative -- Tosoh
Human papillomavirus vaccine TH-GW --	IL-7-Dap 389 fusion toxin -- Ligand
Cantab/GlaxoSmithKline	IM-862 -- Cytran
human polyclonal antibodies -- Biosite/Eos	IMC-1C11 -- ImClone
BioTech./ Medarex	imiglucerase -- Genzyme
human type II anti factor VIII monoclonal	Immune globulin intravenous (human) --
antibodies -- ThromboGenics	Hoffman La Roche
humanised anti glycoprotein Ib murine	immune privilege factor -- Proneuron
monoclonal antibodies -- ThromboGenics	Immunocal -- Immunotec
HumaRAD -- Intracell	Immunogene therapy -- Briana Bio-Tech
HuMax EGFR -- Genmab	Immunoliposomal 5-fluorodeoxyuridine-
HuMax-CD4 -- Medarex	dipalmitate --

FIG. 1N

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immunosuppressant vaccine -- Aixlie	integrin antagonists -- Merck
immunotoxin -- Antisoma, NIH	interferon (Alpha2) -- SRC VB VECTOR,
ImmuRAIT-Re-188 -- Immunomedics	Viragen, Dong-A, Hoffman La-Roche,
imreg-1 -- Imreg	Genentech
infertility -- Johnson & Johnson, E-TRANS	interferon -- BioMedicines, Human Genome
Influenza virus vaccine -- Aventis Pasteur,	Sciences
Protein Sciences	interferon (Alfa-n3)—Interferon Sciences
inhibin -- Biotech Australia, Human	Intl.
Therapeutics	interferon (Alpha), Biphasix -- Helix
Inhibitory G protein gene therapy	interferon (Alpha)—Amgen, BioNative,
INKP-2001 -- InKine	Novartis, Genzyme Transgenics,
Inolimomab -- Diaclone	Hayashibara, Inhale Therapeutics
insulin -- AutoImmune, Altea, Biobras,	Systems, Medusa, Flamel, Dong-A,
BioSante, Bio-Tech. General, Chong Kun	GeneTrol, Nastech, Shantha,
Dang, Emisphere, Flamel, Provalis, Rhein	Wassermann, LG Chem, Sumitomo,
Biotech, TranXenoGen	Aventis, Behring EGIS, Pepgen, Servier,
insulin (bovine) -- Novartis	Rhein Biotech,
insulin analogue -- Eli Lilly	interferon (Alpha2A)
Insulin Aspart -- Novo Nordisk	interferon (Alpha2B) -- Enzon, Schering-
insulin detemir -- Novo Nordisk	Plough, Biogen, IDEA
insulin glargine -- Aventis	interferon (Alpha-N1) -- GlaxoSmithKline
insulin inhaled -- Inhale Therapeutics	interferon (beta) -- Rentschler, GeneTrol,
Systems, Alkermes	Meristem, Rhein Biotech, Toray, Yeda,
insulin oral -- Inovax	Daiichi, Mochida
insulin, AeroDose -- AeroGen	interferon (Beta1A) -- Serono, Biogen
insulin, AERx -- Aradigm	interferon (beta1A), inhale -- Biogen
insulin, BEODAS -- Elan	interferon (β 1b) -- Chiron
insulin, Biphasix -- Helix	interferon (tau) -- Pepgen
insulin, buccal -- Generex	Interferon alfacon-1 -- Amgen
insulin, I2R -- Flemington	Interferon alpha-2a vaccine
insulin, intranasal -- Bentley	Interferon Beta 1b -- Schering/Chiron,
insulin, oral -- Nobex, Unigene	InterMune
insulin, Orasome -- Endorex	Interferon Gamma -- Boehringer Ingelheim,
insulin, ProMaxx -- Epic	Sheffield, Rentschler, Hayashibara
insulin, Quadrant -- Elan	interferon receptor, Type I -- Serono
insulin, recombinant -- Aventis	interferon(Gamma1B) -- Genentech
insulin, Spiros -- Elan	Interferon-alpha-2b + ribavirin -- Biogen,
insulin, Transfersome -- IDEA	ICN
insulin, Zymo, recombinant -- Novo Nordisk	Interferon-alpha-2b gene therapy --
insulinotropin -- Scios	Schering-Plough
Insulysin gene therapy --	Interferon-con1 gene therapy --

FIG. 10

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interleukin-1 antagonists -- Dompe	IPF -- Metabolex
Interleukin-1 receptor antagonist -- Abbott	IR-501 -- Immune Response
Bioresearch, Pharmacia	ISIS 9125 -- Isis Pharmaceuticals
Interleukin-1 receptor type I -- Immunex	ISURF No. 1554 -- Millennium
interleukin-1 receptor Type II -- Immunex	ISURF No. 1866 -- Iowa State Univer.
Interleukin-10 -- DNAX, Schering-Plough	ITF-1697 -- Italfarmaco
Interleukin-10 gene therapy --	IxC 162 -- Ixion
interleukin-12 -- Genetics Institute, Hoffman	J 695 -- Cambridge Antibody Tech.,
La-Roche	Genetics Inst., Knoll
interleukin-13 -- Sanofi	Jagged + FGF -- Repair
interleukin-13 antagonists -- AMRAD	JKC-362 -- Phoenix Pharmaceuticals
Interleukin-13-PE38QQR	JTP-2942 -- Japan Tobacce
interleukin-15 -- Immunex	Juman monoclonal antibodies --
interleukin-16 -- Research Corp	Medarex/Raven
interleukin-18 -- GlaxoSmithKline	K02 -- Axys Pharmaceuticals
Interleukin-1-alpha -- Immunex/Roche	Keliximab -- IDEC
interleukin-2 -- SRC VB VECTOR,	Keyhole limpet haemocyanin
Ajinomoto, Biomira	KGF -- Amgen
Interleukin-3 -- Cangene	KM 871 -- Kyowa
Interleukin-4 -- Immunology Ventures,	KPI 135 -- Scios
Sanofi Winthrop, Schering-Plough,	KPI-022 -- Scios
Immunex/ Sanofi Winthrop, Bayer, Ono	Kringle 5
interleukin-4 + TNF-Alpha -- NIH	KSB 304
interleukin-4 agonist -- Bayer	KSB-201 -- KS Biomedix
interleukin-4 fusion toxin -- Ligand	L 696418 -- Merck
Interleukin-4 receptor -- Immunex, Immun	L 703801 -- Merck
Interleukin-6 -- Ajinomoto, Cangene, Yeda,	L1 -- Acorda
Genetics Institute, Novartis	L-761191 -- Merck
interleukin-6 fusion protein --	lactoferrin -- Meristem, Pharming, Agennix
interleukin-6 fusion toxin -- Ligand, Serono	lactoferrin cardio -- Pharming
interleukin-7 -- IC Innovations	LAG-3 -- Serono
interleukin-7 receptor -- Immunex	LAIT -- GEMMA
interleukin-8 antagonists -- Kyowa	LAK cell cytotoxin -- Arizona
Hakko/Millennium/Pfizer	lamellarins -- PharmaMar/University of
interleukin-9 antagonists -- Genaera	Malaga
Interleukins -- Cel-Sci	laminin A peptides -- NIH
Iodine I 131 tositumomab -- Corixa	lanoteplase -- Genetics Institute
ior EPOCIM -- Center of Molecular	laronidase -- BioMarin
Immunology	Lassa fever vaccine
Ior-P3 -- Center of Molecular Immunology	LCAT -- NIH
IP-10 -- NIH	LDP 01 -- Millennium

FIG. 1P

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LDP 02 -- Millennium
 Lecithinized superoxide dismutase --
 Seikagaku
 LeIF adjuvant --- Corixa
 leishmaniasis vaccine -- Corixa
 lenercept -- Hoffman La-Roche
 Lenograstim -- Aventis, Chugai
 lepirudin -- Aventis
 leptin -- Amgen, IC Innovations
 Leptin gene therapy -- Chiron Corporation
 leptin, 2nd-generation -- Amgen
 leridistim -- Pharmacia
 leuprolide, ProMaxx -- Epic
 leuprorelin, oral -- Unigene
 LeuTech -- Papatin
 LEX 032 -- SuperGen
 LIDEPT -- Novartis
 lipase -- Altus Biologics
 lipid A vaccine -- EntreMed
 lipid-linked anchor Tech. -- ICRT, ID
 Biomedical
 liposome-CD4 Tech. --- Sheffield
 Listeria monocytogenes vaccine
 LMB 1
 LMB 7
 LMB 9 -- Battelle Memorial Institute, NIH
 LM-CD45 --- Cantab Pharmaceuticals
 lovastatin -- Merck
 LSA-3
 LT- β receptor -- Biogen
 lung cancer vaccine -- Corixa
 lusupultide -- Scios
 L-Vax -- AVAX
 LY 355455 -- Eli Lilly
 LY 366405 -- Eli Lilly
 LY-355101 -- Eli Lilly
 Lyme disease DNA vaccine -- Vical/Aventis
 Pasteur
 Lyme disease vaccine -- Aquila
 Biopharmaceuticals, Aventis, Pasteur,
 Symbicom, GlaxoSmithKline, Hyland
 Immuno, MedImmune
 Lymphocytic choriomeningitis virus vaccine
 lymphoma vaccine -- Biomira, Genitope
 LYP18
 lys plasminogen, recombinant
 Lysosomal storage disease gene therapy --
 Avigen
 lysostaphin -- Nutrition 21
 M 23 -- Gruenenthal
 M1 monoclonal antibodies -- Acorda
 Therapeutics
 MA 16N7C2 -- Corvas Intl.
 malaria vaccine -- GlaxoSmithKline,
 AdProTech, Antigenics, Apovia, Aventis
 Pasteur, Axis Genetics, Behringwerke,
 CDCP, Chiron Vaccines, Genzyme
 Transgenics, Hawaii, MedImmune, NIH,
 NYU, Oxxon, Roche/Saramane, Biotech
 Australia, Rx Tech
 Malaria vaccine CDC/NIIMALVAC-1
 malaria vaccine, multicomponent
 mammaglobin -- Corixa
 mammastatin -- Biotherapeutics
 mannan-binding lectin -- NatlImmu
 mannan-MUC1 -- Psiron
 MAP 30
 Marinovir -- Phytera
 MARstem -- Maret
 MB-015 -- Mochida
 MBP -- ImmuLogic
 MCI-028 --- Mitsubishi-Tokyo
 MCIF -- Human Genome Sciences
 MDC -- Advanced BioScience -- Akzo
 Nobel, ICOS
 MDX 11 -- Medarex
 MDX 210 -- Medarex
 MDX 22 -- Medarex
 MDX 22

FIG. 1Q

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MDX 240 -- Medarex	Methionine lyase gene therapy --
MDX 33	AntiCancer
MDX 44 -- Medarex	Met-RANTES -- Genexa Biomedical,
MDX 447 -- Medarex	Serono
MDX H210 -- Medarex	Metreleptin
MDX RA -- Houston BioTech., Medarex	MGDF -- Kirin
ME-104 -- Pharmexa	MGV -- Progenics
Measles vaccine	micrin -- Endocrine
Mecasemin -- Cephalon/Chiron, Chiron	microplasmin -- ThromboGenics
MEDI 488 -- MedImmune	MIF -- Genetics Institute
MEDI 500	migration inhibitory factor -- NIH
MEDI 507 -- BioTransplant	Mim CD4.1 -- Xycte Therapies
melanin concentrating hormone --	mirostipen -- Human Genome Sciences
Neurocrine Biosciences	MK 852 -- Merck
melanocortins -- OMRF	Mobenakin -- NIS
Melanoma monoclonal antibodies -- Viragen	molgramostim -- Genetics Institute, Novartis
melanoma vaccine -- GlaxoSmithKline,	monoclonal antibodies -- Abgenix/Celltech,
Akzo Nobel, Avant, Aventis Pasteur,	Immusol/ Medarex, Viragen/ Roslin
Bavarian Nordic, Biovector, CancerVax,	Institute, Cambridge Antibody Tech./Elan
Genzyme Molecular Oncology, Humbolt,	MAb 108 --
ImClone Systems, Memorial, NYU, Oxxon	MAb 10D5 --
Melanoma vaccine Magevac -- Therion	MAb 14.18-interleukin-2 immunocytokine --
memory enhancers -- Scios	Lexigen
meningococcal B vaccine -- Chiron	MAb 14G2a --
meningococcal vaccine -- CAMR	MAb 15A10 --
Meningococcal vaccine group B conjugate -	MAb 170 -- Biomira
- North American Vaccine	MAb 177Lu CC49 --
Meningococcal vaccine group B	MAb 17F9
recombinant -- BioChem Vaccines,	MAb 1D7
Microscience	MAb 1F7 -- Immune Network
Meningococcal vaccine group Y conjugate -	MAb 1H10-doxorubicin conjugate
- North American Vaccine	MAb 26-2F
Meningococcal vaccine groups A B and C	MAb 2A11
conjugate -- North American Vaccine	MAb 2E1 -- RW Johnson
Mepolizumab -- GlaxoSmithKline	MAb 2F5
Metastatin -- EntreMed, Takeda	MAb 31.1 -- International BioImmune
Met-CkB7 -- Human Genome Sciences	Systems
met-enkephalin -- TNI	MAb 32 -- Cambridge Antibody Tech.,
METH-1 -- Human Genome Sciences	Peptech
methioninase -- AntiCancer	MAb 323A3 -- Centocor
	MAb 3C5

FIG. 1R

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MAb 3F12	MAb C242-PE conjugate
MAb 3F8	MAb c30-6
MAb 42/6	MAb CA208-cytorhodin-S conjugate --
MAb 425 -- Merck KGaA	Hoechst Japan
MAb 447-52D -- Merck Sharp & Dohme	MAb CC49 -- Enzon
MAb 45-2D9- -- haematoporphyrin	MAb ch14.18 --
conjugate	MAb CH14.18-GM-CSF fusion protein --
MAb 4B4	Lexigen
MAb 4E3-CPA conjugate -- BCM Oncologia	MAb chCE7
MAb 4E3-daunorubicin conjugate	MAb CI-137 -- AMRAD
MAb 50-6	MAb cisplatin conjugate
MAb 50-61A -- Institut Pasteur	MAb CLB-CD19
MAb 5A8 -- Biogen	MAb CLB-CD19v
MAb 791T/36-methotrexate conjugate	MAb CLL-1 -- Peregrine
MAb 7c11.e8	MAb CLL-1-GM-CSF conjugate
MAb 7E11 C5-selenocystamine conjugate	MAb CLL-1-IL-2 conjugate -- Peregrine
MAb 93KA9 -- Novartis	MAb CLN IgG -- doxorubicin conjugates
MAb A5B7-cisplatin conjugate --	MAb conjugates -- Tanox
Biodynamics Research, Pharmacia	MAb D612
MAb A5B7-I-131	MAb Dal B02
MAb A7	MAb DC101 -- ImClone
MAb A717 -- Exocell	MAb EA 1 --
MAb A7-zinostatin conjugate	MAb EC708 -- Biovation
MAb ABX-RB2 -- Abgenix	MAb EP-5C7 -- Protein Design Labs
MAb ACA 11	MAb ERIC-1 -- ICRT
MAb AFP-I-131 -- Immunomedics	MAb F105 gene therapy
MAb AP1	MAb FC 2.15
MAb AZ1	MAb G250 -- Centocor
MAb B3-LysPE40 conjugate	MAb GA6
MAb B4 -- United Biomedical	MAb GA733
MAb B43 Genistein-conjugate	MAb Gliomab-H -- Viventia Biotech
MAb B43.13-Tc-99m -- Biomira	MAb HB2-saporin conjugate
MAb B43-PAP conjugate	MAb HD 37 --
MAb B4G7-gelonin conjugate	MAb HD37-ricin chain-A conjugate
MAb BCM 43-daunorubicin conjugate --	MAb HNK20 -- Acambis
BCM Oncologia	MAb huN901-DM1 conjugate --
MAb BIS-1	ImmunoGen
MAb BMS 181170 -- Bristol-Myers Squibb	MAb I-131 CC49 -- Corixa
MAb BR55-2	MAb ICO25
MAb BW494	MAb ICR12-CPG2 conjugate
MAb C 242-DM1 conjugate -- ImmunoGen	MAb ICR-62

FIG. 1S

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MAB IRac-ricin A conjugate	MAB R-24
MAB K1	MAB R-24 α Human GD3 -- Celltech
MAB KS1-4-methotrexate conjugate	MAB RFB4-ricin chain A conjugate
MAB L6 -- Bristol-Myers Squibb, Oncogen	MAB RFT5-ricin chain A conjugate
MAB LiCO 16-88	MAB SC 1
MAB LL2-I-131 -- Immunomedics	MAB SM-3 -- ICRT
MAB LL2-Y-90	MAB SMART 1D10 -- Protein Design Labs
MAB LS2D617 -- Hybritech	MAB SMART ABL 364 -- Novartis
MAB LYM-1-gelonin conjugate	MAB SN6f
MAB LYM-1-I-131	MAB SN6f-deglycosylated ricin A chain
MAB LYM-1-Y-90	conjugate --
MAB LYM-2 -- Peregrine	MAB SN6j
MAB M195	MAB SN7-ricin chain A conjugate
MAB M195-bismuth 213 conjugate --	MAB T101-Y-90 conjugate -- Hybritech
Protein Design Labs	MAB T-88 -- Chiron
MAB M195-gelonin conjugate	MAB TB94 -- Cancer ImmunoBiology
MAB M195-I-131	MAB TEC 11
MAB M195-Y-90	MAB TES-23 -- Chugai
MAB MA 33H1 -- Sanofi	MAB TM31 -- Avant
MAB MAD11	MAB TNT-1 -- Cambridge Antibody Tech.,
MAB MGB2	Peregrine
MAB MINT5	MAB TNT-3
MAB MK2-23	MAB TNT-3 -- IL2 fusion protein --
MAB MOC31 ETA(252-613) conjugate	MAB TP3-At-211
MAB MOC-31-In-111	MAB TP3-PAP conjugate --
MAB MOC-31-PE conjugate	MAB UJ13A -- ICRT
MAB MR6 --	MAB UN3
MAB MRK-16 -- Aventis Pasteur	MAB ZME-018-gelonin conjugate
MAB MS11G6	MAB-BC2 -- GlaxoSmithKline
MAB MX-DTPA BrE-3	MAB-DM1 conjugate -- ImmunoGen
MAB MY9	MAB-ricin-chain-A conjugate -- XOMA
MAB Nd2 -- Tosoh	MAB-temoporfin conjugates
MAB NG-1 -- Hygeia	Monopharm C -- Viventia Biotech
MAB NM01 -- Nissin Food	monteplase -- Eisai
MAB OC 125	montirelin hydrate -- Gruenenthal
MAB OC 125-CMA conjugate	moroctocog alfa -- Genetics Institute
MAB OKI-1 -- Ortho-McNeil	Moroctocog-alfa -- Pharmacia
MAB OX52 -- Bioproducts for Science	MP 4
MAB PMA5	MP-121 -- Biopharm
MAB PR1	MP-52 -- Biopharm
MAB prost 30	MRA -- Chugai

FIG. 1T

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MS 28168 -- Mitsui Chemicals, Nihon Schering	Neuroprotective vaccine -- University of Auckland
MSH fusion toxin -- Ligand	neurotrophic chimaeras -- Regeneron
MSI-99 -- Genaera	neurotrophic factor -- NsGene, CereMedix
MT 201 -- Micromet	NeuroVax -- Immune Response
Muc-1 vaccine -- Corixa	neurturin -- Genentech
mucosal tolerance -- Aberdeen	neutral endopeptidase -- Genentech
mullerian inhibiting subst	NGF enhancers -- NeuroSearch
muplestim -- Genetics Institute, Novartis, DSM Anti-Infectives	NHL vaccine -- Large Scale Biology
murine MAb -- KS Biomedix	NIP45 -- Boston Life Sciences
Mutant somatropin -- JCR Pharmaceutical	NKI-B20
MV 833 -- Toagosei	NM 01 -- Nissin Food
Mycoplasma pulmonis vaccine	NMI-139 -- NitroMed
Mycoprex -- XOMA	NMMP -- Genetics Institute
myeloperoxidase -- Henogen	NN-2211 -- Novo Nordisk
myostatin -- Genetics Institute	Noggin -- Regeneron
Nacolomab tafenatox -- Pharmacia	Nonacog alfa
nagrestipen -- British Biotech	Norelin -- Biostar
NAP-5 -- Corvas Intl.	Norwalk virus vaccine
NAPc2 -- Corvas Intl.	NRLU 10 -- NeoRx
nartograstim -- Kyowa	NRLU 10 PE -- NeoRx
Natalizumab -- Protein Design Labs	NT-3 -- Regeneron
Nateplase -- NIH, Nihon Schering	NT-4/5 -- Genentech
nateplase -- Schering AG	NU 3056
NBI-3001 -- Neurocrine Biosci.	NU 3076
NBI-5788 -- Neurocrine Biosci.	NX 1838 -- Gilead Sciences
NBI-6024 -- Neurocrine Biosci.	NY ESO-1/CAG-3 antigen -- NIH
Nef inhibitors -- BRI	NYVAC-7 -- Aventis Pasteur
Neisseria gonorrhoea vaccine -- Antex Biologics	NZ-1002 -- Novazyme
Neomycin B-arginine conjugate	obesity therapy -- Nobex
Nerelimomab -- Chiron	OC 10426 -- Ontogen
Nerve growth factor -- Amgen -- Chiron, Genentech	OC 144093 -- Ontogen
Nerve growth factor gene therapy	OCIF -- Sankyo
nesiritide citrate -- Scios	Oct-43 -- Otsuka
neuregulin-2 -- CeNeS	OK PSA - liposomal
neurocan -- NYU	OKT3-gamma-1-ala-ala
neuronal delivery system -- CAMR	OM 991
	OM 992
	Omalizumab -- Genentech
	oncoimmunin-L -- NIH
	Oncolysin B -- ImmunoGen

FIG. 1U

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Oncolysin CD6 -- ImmunoGen	PAM 4 -- Merck
Oncolysin M -- ImmunoGen	pamiteplase -- Yamanouchi
Oncolysin S -- ImmunoGen	pancreatin, Minitabs -- Eurand
Oncophage -- Antigenics	Pangen -- Fournier
Oncostatin M -- Bristol-Myers Squibb	Pantarin -- Selective Genetics
OncoVax-CL -- Jenner Biotherapies	Parainfluenza virus vaccine -- Pharmacia,
OncoVax-P -- Jenner Biotherapies	Pierre Fabre
onercept -- Yeda	paraoxanase -- Esperion
onychomycosis vaccine -- Boehringer	parathyroid hormone -- Abiogen, Korea
Ingelheim	Green Cross
opebecan -- XOMA	Parathyroid hormone (1-34) --
opioids -- Arizona	Chugai/Suntory
Oprelvekin -- Genetics Institute	Parkinson's disease gene therapy -- Cell
Org-33408 b-- Akzo Nobel	Genesys/ Ceregene
Orolip DP -- EpiCept	Parvovirus vaccine -- MedImmune
oryzacyclatin	PCP-Scan -- Immunomedics
OSA peptides -- GenSci Regeneration	PDGF cocktail -- Theratechnologies
osteoblast-cadherin GF -- Pharis	peanut allergy therapy -- Dynavax
Osteocalcin-thymidine kinase gene therapy	PEG anti-ICAM MAb -- Boehringer
osteogenic protein -- Curis	Ingelheim
osteopontin -- OraPharma	PEG asparaginase -- Enzon
osteoporosis peptides -- Integra, Telios	PEG glucocerebrosidase
osteoprotegerin -- Amgen, SnowBrand	PEG hirudin -- Knoll
otitis media vaccines -- Antex Biologics	PEG interferon-alpha-2a -- Roche
ovarian cancer -- University of Alabama	PEG interferon-alpha-2b + ribavirin --
OX40-IgG fusion protein -- Cantab, Xenova	Biogen, Enzon, ICN Pharmaceuticals,
P 246 -- Diatide	Schering-Plough
P 30 -- Alfacell	PEG MAb A5B7 --
p1025 -- Active Biotech	Pegacaristim -- Amgen -- Kirin Brewery --
P-113 ^A -- Demegen	ZymoGenetics
P-16 peptide -- Transition Therapeutics	Pegaldesleukin -- Research Corp
p43 -- Ramot	pegaspargase -- Enzon
P-50 peptide -- Transition Therapeutics	pegfilgrastim -- Amgen
p53 + RAS vaccine -- NIH, NCI	PEG-interferon Alpha -- Viragen
PACAP(1-27) analogue	PEG-interferon Alpha 2A -- Hoffman La-
paediatric vaccines -- Chiron	Roche
Pafase -- ICOS	PEG-interferon Alpha 2B -- Schering-
PAGE-4 plasmid DNA -- IDEC	Plough
PAI-2 -- Biotech Australia, Human	PEG-r-hirudin -- Abbott
Therapeutics	PEG-uricase -- Mountain View
Palivizumab -- MedImmune	Pegvisomant -- Genentech

FIG. 1V

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PEGylated proteins, PolyMASC -- Valentis Pharmaprojects No. 5947 -- StressGen
 PEGylated recombinant native human leptin Pharmaprojects No. 5961 --
 -- Roche Theratechnologies
 Pemtumomab Pharmaprojects No. 5962 -- NIH
 Penetratin -- Cyclacel Pharmaprojects No. 5966 -- NIH
 Pepscan -- Antisoma Pharmaprojects No. 5994 -- Pharming
 peptide G -- Peptech, ICRT Pharmaprojects No. 5995 -- Pharming
 peptide vaccine -- NIH, NCI Pharmaprojects No. 6023 -- IMMUCON
 Pexelizumab Pharmaprojects No. 6063 -- Cytoclonal
 pexiganan acetate -- Genaera Pharmaprojects No. 6073 -- SIDDCO
 Pharmaprojects No. 3179 -- NYU Pharmaprojects No. 6115 -- Genzyme
 Pharmaprojects No. 3390 -- Ernest Orlando Pharmaprojects No. 6227 -- NIH
 Pharmaprojects No. 3417 -- Sumitomo Pharmaprojects No. 6230 -- NIH
 Pharmaprojects No. 3777 -- Acambis Pharmaprojects No. 6236 -- NIH
 Pharmaprojects No. 4209 -- XOMA Pharmaprojects No. 6243 -- NIH
 Pharmaprojects No. 4349 -- Baxter Intl. Pharmaprojects No. 6244 -- NIH
 Pharmaprojects No. 4651 Pharmaprojects No. 6281 -- Senetek
 Pharmaprojects No. 4915 -- Avanir Pharmaprojects No. 6365 -- NIH
 Pharmaprojects No. 5156 -- Rhizogenics Pharmaprojects No. 6368 -- NIH
 Pharmaprojects No. 5200 -- Pfizer Pharmaprojects No. 6373 -- NIH
 Pharmaprojects No. 5215 -- Origene Pharmaprojects No. 6408 -- Pan Pacific
 Pharmaprojects No. 5216 -- Origene Pharmaprojects No. 6410 -- Athersys
 Pharmaprojects No. 5218 -- Origene Pharmaprojects No. 6421 -- Oxford
 Pharmaprojects No. 5267 -- ML GlycoSciences
 Laboratories Pharmaprojects No. 6522 -- Maxygen
 Pharmaprojects No. 5373 -- MorphoSys Pharmaprojects No. 6523 -- Pharis
 Pharmaprojects No. 5493 -- Metabolex Pharmaprojects No. 6538 -- Maxygen
 Pharmaprojects No. 5707 -- Genentech Pharmaprojects No. 6554 -- APALEXO
 Pharmaprojects No. 5728 -- Autogen Pharmaprojects No. 6560 -- Ardana
 Pharmaprojects No. 5733 -- BioMarin Pharmaprojects No. 6562 -- Bayer
 Pharmaprojects No. 5757 -- NIH Pharmaprojects No. 6569 -- Eos
 Pharmaprojects No. 5765 -- Gryphon Phenoxazine
 Pharmaprojects No. 5830 -- AntiCancer Phenylase -- Ibex
 Pharmaprojects No. 5839 -- Dyax Pigment epithelium derived factor --
 Pharmaprojects No. 5849 -- Johnson & plasminogen activator inhibitor-1,
 Johnson recombinant -- DuPont Pharmaceuticals
 Pharmaprojects No. 5860 -- Mitsubishi-
 Tokyo
 Pharmaprojects No. 5869 -- Oxford
 GlycoSciences
 Pharmaprojects No. 5883 -- Asahi Brewery

FIG. 1W

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Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda	prostate-specific antigen -- EntreMed
plasminogen-related peptides -- Bio-Tech. General/MGH	protein A -- RepliGen
platelet factor 4 -- RepliGen	protein adhesives -- Enzon
Platelet-derived growth factor -- Amgen -- ZymoGenetics	protein C -- Baxter Intl., PPL Therapeutics, ZymoGenetics
plusonemin-- Hayashibara	protein C activator -- Gilead Sciences
PMD-2850 -- Protherics	protein kinase R antags -- NIH
Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur	protirelin -- Takeda
Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector	protocadherin 2 -- Caprion
PR1A3	Pro-urokinase -- Abbott, Bristol-Myers Squibb, Dainippon, Tosoh -- Welfide
PR-39	P-selectin glycoprotein ligand-1 -- Genetics Institute
pralmorelin -- Kaken	pseudomonal infections -- InterMune
Pretarget-Lymphoma -- NeoRx	Pseudomonas vaccine -- Cytovax
Priliximab -- Centocor	PSGL-Ig -- American Home Products
PRO 140 -- Progenics	PSP-94 -- Procyon
PRO 2000 -- Procept	PTH 1-34 -- Nobex
PRO 367 -- Progenics	Quilimmune-M -- Antigenics
PRO 542 -- Progenics	R 101933
pro-Apo A-I -- Esperion	R 125224 -- Sankyo
prolactin -- Genzyme	RA therapy -- Cardion
Prosaptide TX14(A) -- Bio-Tech. General	Rabies vaccine recombinant -- Aventis Pasteur, BioChem Vaccines, Kaketsuken Pharmaceuticals
prostate cancer antibodies -- Immunex, UroCor	RadioTheraCIM -- YM BioSciences
prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics	Ramot project No. 1315 -- Ramot
prostate cancer immunotherapeutics -- The PSMA Development Company	Ramot project No. K-734A -- Ramot
prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner Biotherapies, Therion Biologics	Ramot project No. K-734B -- Ramot
	RANK -- Immunex
	ranpirinase -- Alfacell
	ranpirinase-anti-CD22 MAb -- Alfacell
	RANTES inhibitor -- Milan
	RAPID drug delivery systems -- ARIAD
	rasburicase -- Sanofi
	rBPI-21, topical -- XOMA
	RC 529 -- Corixa
	rCFTR -- Genzyme Transgenics
	RD 62198
	rDnase -- Genentech
	RDP-58 -- SangStat

FIG. 1X

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RecepTox-Fce -- Keryx	Ribozyme gene therapy -- Genset
RecepTox-GnRH -- Keryx, MTR Technologies	Rickettsial vaccine recombinant
RecepTox-MBP -- Keryx, MTR Technologies	RIGScan CR -- Neoprobe
recFSH -- Akzo Nobel, Organon	RIP-3 -- Rigel
REGA 3G12	RK-0202 -- RxKinetix
Regavirumab -- Teijin	RLT peptide -- Esperion
relaxin -- Connetics Corp	rM/NEI -- IVAX
Renal cancer vaccine -- Macropharm	rmCRP -- Immtech
repifermin -- Human Genome Sciences	RN-1001 -- Renovo
Respiratory syncytial virus PFP-2 vaccine -- Wyeth-Lederle	RN-3 -- Renovo
Respiratory syncytial virus vaccine -- GlaxoSmithKline, Pharmacia, Pierre Fabre	RNAse conjugate -- Immunomedics
Respiratory syncytial virus vaccine inactivated	RO 631908 -- Roche
Respiratory syncytial virus-parainfluenza virus vaccine -- Aventis Pasteur, Pharmacia	Rotavirus vaccine -- Merck
Reteplase -- Boehringer Mannheim, Hoffman La-Roche	RP 431 -- DuPont Pharmaceuticals
Retropep -- Retroscreen	RP-128 -- Resolution
RFB4 (dsFv) PE38	RPE65 gene therapy --
RFI 641 -- American Home Products	RPR 110173 -- Aventis Pasteur
RFTS -- UAB Research Foundation	RPR 115135 -- Aventis Pasteur
RG 12986 -- Aventis Pasteur	RPR 116258A -- Aventis Pasteur
RG 83852 -- Aventis Pasteur	rPSGL-Ig -- American Home Products
RG-1059 -- RepliGen	r-SPC surfactant -- Byk Gulden
rGCR -- NIH	rV-HER-2/neu -- Therion Biologics
rGLP-1 -- Restoragen	SA 1042 -- Sankyo
rGRF -- Restoragen	sacrosidase -- Orphan Medical
rh Insulin -- Eli Lilly	Sant 7
RHAMM targeting peptides -- Cangene	Sargramostim -- Immunex
rHb1.1 -- Baxter Intl.	saruplase -- Gruenenthal
rhCC10 -- Claragen	Satumomab -- Cytogen
rhCG -- Serono	SB 1 -- COR Therapeutics
Rheumatoid arthritis gene therapy	SB 207448 -- GlaxoSmithKline
Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center	SB 208651 -- GlaxoSmithKline
rhLH -- Serono	SB 240683 -- GlaxoSmithKline
	SB 249415 -- GlaxoSmithKline
	SB 249417 -- GlaxoSmithKline
	SB 6 -- COR Therapeutics
	SB RA 31012 --
	SC 56929 -- Pharmacia
	SCA binding proteins -- Curis, Enzon
	scFv(14E1)-ETA Berlex Laboratories, Schering AG
	ScFv(FRP5)-ETA --

FIG. 1Y

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ScFv6C6-PE40 --	somatomedin-1 -- GroPep, Mitsubishi-Tokyo, NIH
SCH 55700 -- Celltech	somatomedin-1 carrier protein -- Insmed
Schistosomiasis vaccine -- Glaxo Wellcome/Medeira, Brazil	somatostatin -- Ferring
SCPF -- Advanced Tissue Sciences	Somatotropin/
scuPA-suPAR complex -- Hadasit	Human Growth Hormone -- Bio-Tech. General, Eli Lilly
SD-9427 -- Pharmacia	somatropin -- Bio-Tech. General, Alkermes, ProLease, Aventis Behring, Biovector, Cangene, Dong-A, Eli Lilly, Emisphere, Enact, Genentech, Genzyme Transgenics, Grandis/InfiMed, CSL, InfiMed, MacroMed, Novartis, Novo Nordisk, Pharmacia
SDF-1 -- Ono	Serono, TranXenoGen
SDZ 215918 -- Novartis	somatropin derivative -- Schering AG
SDZ 280125 -- Novartis	somatropin, AIR -- Eli Lilly
SDZ 89104 -- Novartis	Somatropin, inhaled -- Eli Lilly/Alkermes
SDZ ABL 364 -- Novartis	somatropin, Kabi -- Pharmacia
SDZ MMA 383 -- Novartis	somatropin, Orasome -- Novo Nordisk
serine protease inhibs -- Pharis	Sonermin -- Dainippon Pharmaceutical
sermorelin acetate -- Serono	SP(V5.2)C -- Supertek
SERP-1 -- Viron	SPf66
sertenef -- Dainippon	sphingomyelinase -- Genzyme
serum albumin, Recombinant human -- Aventis Behring	SR 29001 -- Sanofi
serum-derived factor -- Hadasit	SR 41476 -- Sanofi
Sevirumab -- Novartis	SR-29001 -- Sanofi
SGN 14 -- Seattle Genetics	SS1(dsFV)-PE38 -- NeoPharm
SGN 15 -- Seattle Genetics	β 2 microglobulin -- Avidex
SGN 17/19 -- Seattle Genetics	β 2-microglobulin fusion proteins -- NIH
SGN 30 -- Seattle Genetics	β -amyloid peptides -- CeNeS
SGN-10 -- Seattle Genetics	β -defensin -- Pharis
SGN-11 -- Seattle Genetics	Staphylococcus aureus infections -- Inhibitex/ZLB
SH 306 -- DuPont Pharmaceuticals	Staphylococcus aureus vaccine conjugate -- Nabi
Shanvac-B -- Shantha	Staphylococcus therapy -- Tripep
Shigella flexneri vaccine -- Avant, Acambis, Novavax	Staphylokinase -- Biovation, Prothera, Thrombogenetics
Shigella sonnei vaccine --	Streptococcal A vaccine -- M6
sICAM-1 -- Boehringer Ingelheim	Pharmaceuticals, North American Vaccine
Silteplase -- Genzyme	Streptococcal B vaccine -- Microscience
SIV vaccine -- Endocon, Institut Pasteur	
SK 896 -- Sanwa Kagaku Kenkyusho	
SK-827 -- Sanwa Kagaku Kenkyusho	
Skeletex -- CellFactors	
SKF 106160 -- GlaxoSmithKline	
S-nitroso-AR545C --	
SNTP -- Active Biotech	

FIG. 1Z

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Streptococcal B vaccine recombinant -- Biochem Vaccines	TFPI -- EntreMed
Streptococcus pyogenes vaccine	tgD-IL-2 -- Takeda
STRL-33 -- NIH	TGF-Alpha -- ZymoGenetics
Subalin -- SRC VB VECTOR	TGF- β -- Kolon
SUIS -- United Biomedical	TGF- β 2 -- Insmed
SUIS-LHRH -- United Biomedical	TGF- β 3 -- OSI
SUN-E3001 -- Suntory	Thalassaemia gene therapy -- Crucell
super high affinity monoclonal antibodies -- YM BioSciences	TheraCIM-h-R3 -- Center of Molecular Immunology, YM BioSciences
Superoxide dismutase -- Chiron, Enzon, Ube Industries, Bio-Tech, Yeda	Theradigm-HBV -- Epimmune
superoxide dismutase-2 -- OXIS	Theradigm-HPV -- Epimmune
suppressin -- UAB Research Foundation	Theradigm-malaria -- Epimmune
SY-161-P5 -- ThromboGenics	Theradigm-melanoma -- Epimmune
SY-162 -- ThromboGenics	TheraFab -- Antisoma
Systemic lupus erythematosus vaccine -- MedClone/VivoRx	ThGRF 1-29 -- Theratechnologies
T cell receptor peptide vaccine	ThGRF 1-44 -- Theratechnologies
T4N5 liposomes -- AGI Dermatics	thrombomodulin -- Iowa, Novocastra
TACI, soluble -- ZymoGenetics	Thrombopoietin -- Dragon Pharmaceuticals, Genentech
targeted apoptosis -- Antisoma	thrombopoietin, Pliva -- Recepton
tasonermin -- Boehringer Ingelheim	Thrombospondin 2 --
TASP	thrombostatin -- Thromgen
TASP-V	thymalfasin -- SciClone
Tat peptide analogues -- NIH	thymocartin -- Gedeon Richter
TBP I -- Yeda	thymosin Alpha1 -- NIH
TBP II	thyroid stimulating hormone -- Genzyme
TBV25H -- NIH	tICAM-1 -- Bayer
Tc 99m lor cea1 -- Center of Molecular Immunology	Tick anticoagulant peptide -- Merck
Tc 99m P 748 -- Diatide	TIF -- Xoma
Tc 99m votumumab -- Intracell	Tifacogin -- Chiron, NIS, Pharmacia
Tc-99m rh-Annexin V -- Theseus Imaging	Tissue factor -- Genentech
teceleukin -- Biogen	Tissue factor pathway inhibitor
tenecteplase -- Genentech	TJN-135 -- Tsumura
Teriparatide -- Armour Pharmaceuticals, Asahi Kasei, Eli Lilly	TM 27 -- Avant
terlipressin -- Ferring	TM 29 -- Avant
testisin -- AMRAD	TMC-151 -- Tanabe Seiyaku
Tetrafibricin -- Roche	TNF tumour necrosis factor -- Asahi Kasei
	TNF Alpha -- CytImmune
	TNF antibody -- Johnson & Johnson
	TNF binding protein -- Amgen
	TNF degradation product -- Oncotech

FIG. 1AA

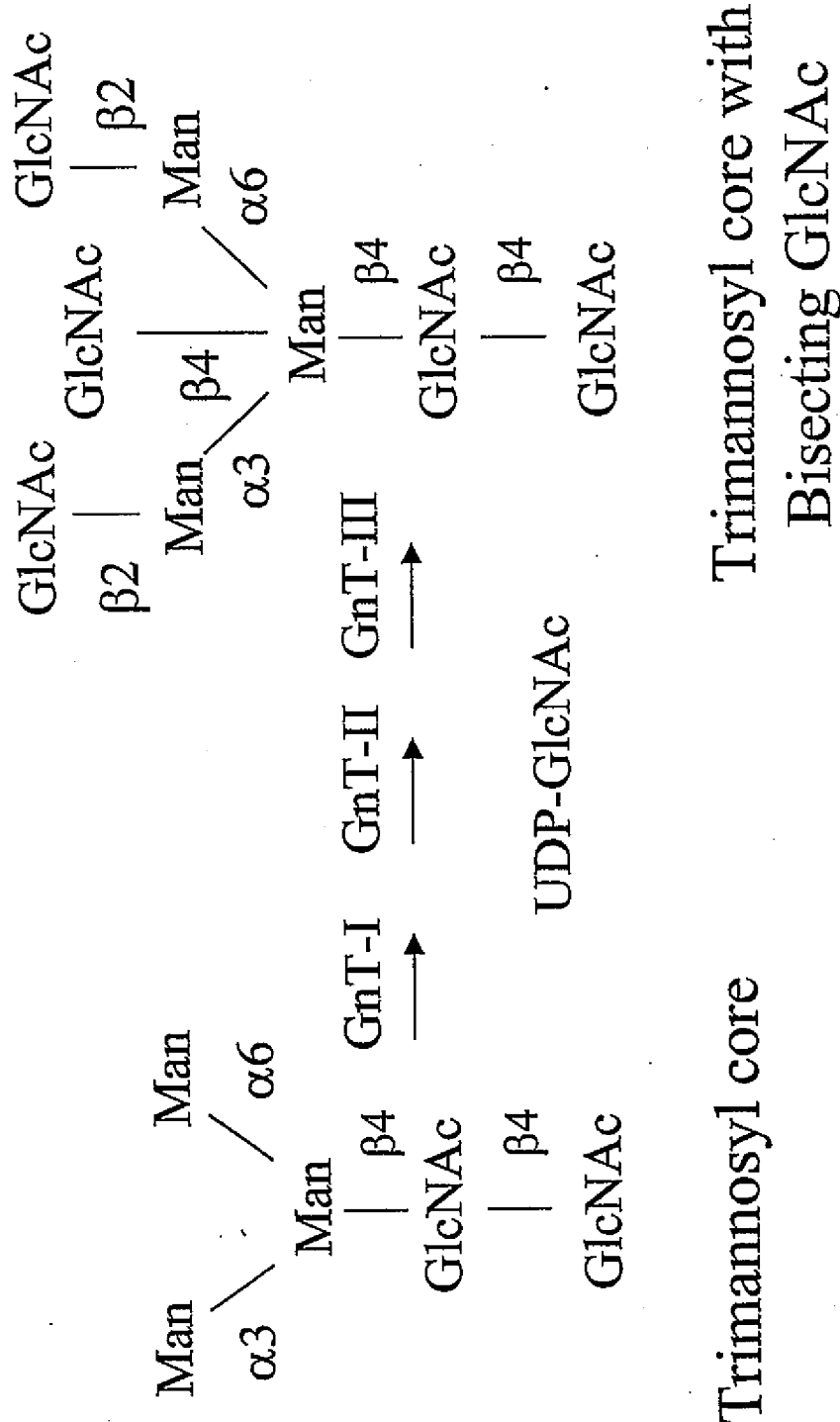
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TNF receptor -- Immunex	TXU-PAP
TNF receptor 1, soluble -- Amgen	TY-10721 -- TOA Eiyo
TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genetech, Mochida	Type I diabetes vaccine -- Research Corp
TNF-Alpha inhibitor -- Tripep	Typhoid vaccine CVD 908
TNFR:Fc gene therapy -- Targeted Genetics	U 143677 -- Pharmacia
TNF-SAM2	U 81749 -- Pharmacia
Tolerimab -- Innogenetics	UA 1248 -- Arizona
Toxoplasma gondii vaccine -- GlaxoSmithKline	UGIF -- Sheffield
TP 9201 -- Telios	UIC 2
TP10 -- Avant	UK 101
TP20 -- Avant	UK-279276 -- Corvas Intl.
tPA -- Centocor	urodilatin -- Pharis
trafermin -- Scios	urofolitrophin -- Serono
TRAIL/Apo2L -- Immunex	uteroferrin -- Pepgen
transferrin-binding proteins -- CAMR	V 20 -- GLYCODESIGN
Transforming growth factor-beta-1 -- Genentech	V2 vasopressin receptor gene therapy
transport protein -- Genesis	vaccines -- Active Biotech
TRH -- Ferring	Varicella zoster glycoprotein vaccine -- Research Corporation Technologies
Triabin -- Schering AG	Varicella zoster virus vaccine live -- Cantab Pharmaceuticals
Triconal	Vascular endothelial growth factor -- Genentech, University of California
Triflavin	Vascular endothelial growth factors -- R&D Systems
troponin I -- Boston Life Sciences	vascular targeting agents -- Peregrine
TRP-2 ^h -- NIH	vasopermeation enhancement agents -- Peregrine
trypsin inhibitor -- Mochida	vasostatin -- NIH
TSP-1 gene therapy --	VCL -- Bio-Tech. General
TT-232	VEGF -- Genentech, Scios
TTS-CD2 -- Active Biotech	VEGF inhibitor -- Chugai
Tuberculosis vaccine -- Aventis Pasteur, Genesis	VEGF-2 -- Human Genome Sciences
Tumor Targeted Superantigens -- Active Biotech -- Pharmacia	VEGF-Trap -- Regeneron
tumour vaccines -- PhotoCure	viscumin, recombinant -- Madaus
tumour-activated prodrug antibody conjugates -- Millennium/ImmunoGen	Vitaxin
tumstatin -- ILEX	Vitrax -- ISTA Pharmaceuticals
Tuvirumab -- Novartis	West Nile virus vaccine -- Bavarian Nordic
TV-4710 -- Teva	WP 652
TWEAK receptor -- Immunex	WT1 vaccine -- Corixa
	WX-293 -- Willex BioTech.

FIG. 1BB

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WX-360 -- Wilex BioTech.	YM 207 -- Yamanouchi
WX-UK1 -- Wilex BioTech.	YM 337 -- Protein Design Labs
XMP-500 -- XOMA	Yttrium-90 labelled biotin
XomaZyme-791 -- XOMA	Yttrium-90-labeled anti-CEA MAb T84.66 --
XTL 001 -- XTL Biopharmaceuticals	ZD 0490 -- AstraZeneca
XTL 002 -- XTL Biopharmaceuticals	ziconotide -- Elan
yeast delivery system -- GlobelImmune	ZK 157138 -- Berlex Laboratories
Yersinia pestis vaccine	Zolimomab aritox
YIGSR-Stealth -- Johnson & Johnson	Zorcell -- Immune Response
Yisum Project No. D-0460 -- Yisum	ZRXL peptides -- Novartis



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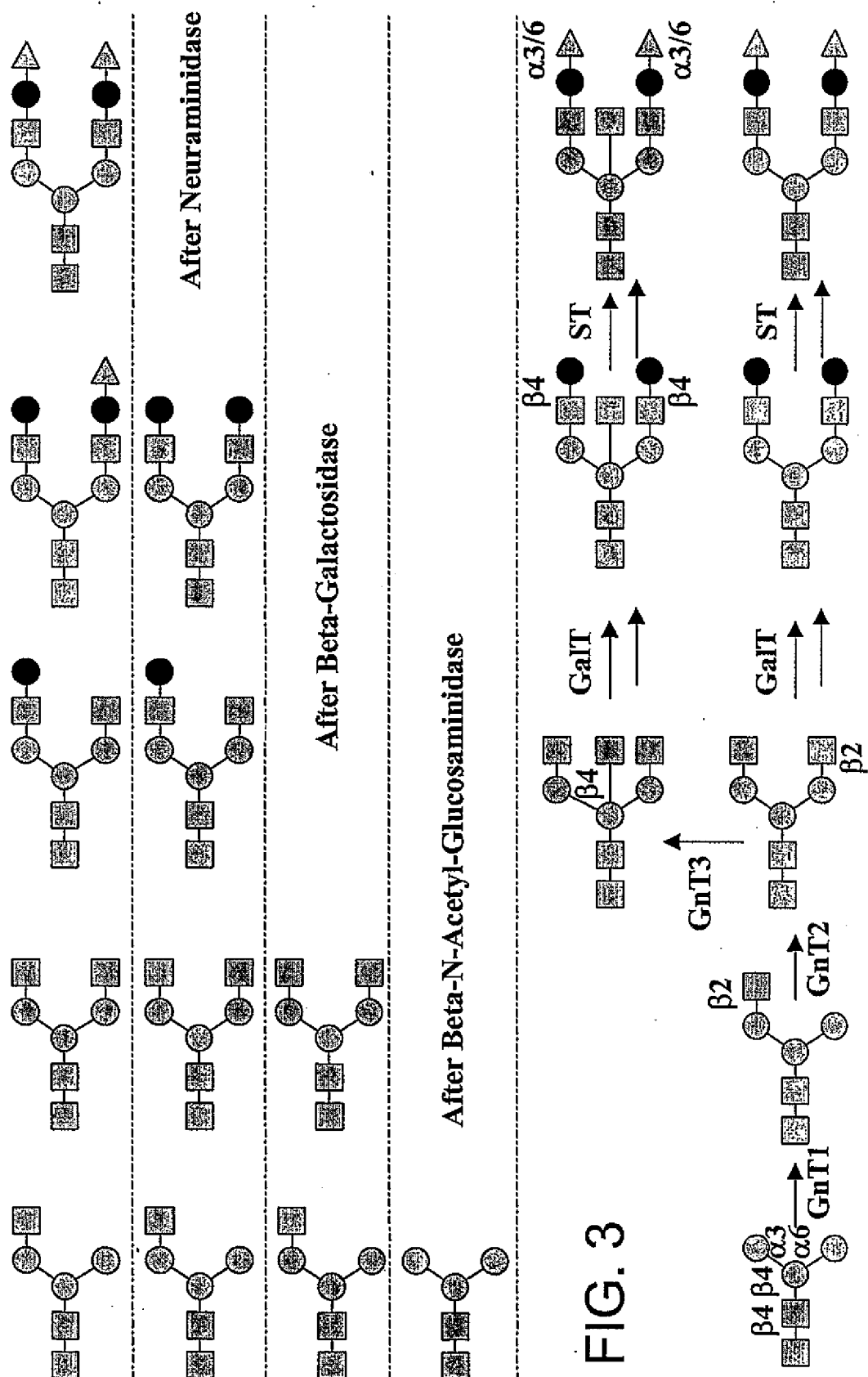


FIG. 3

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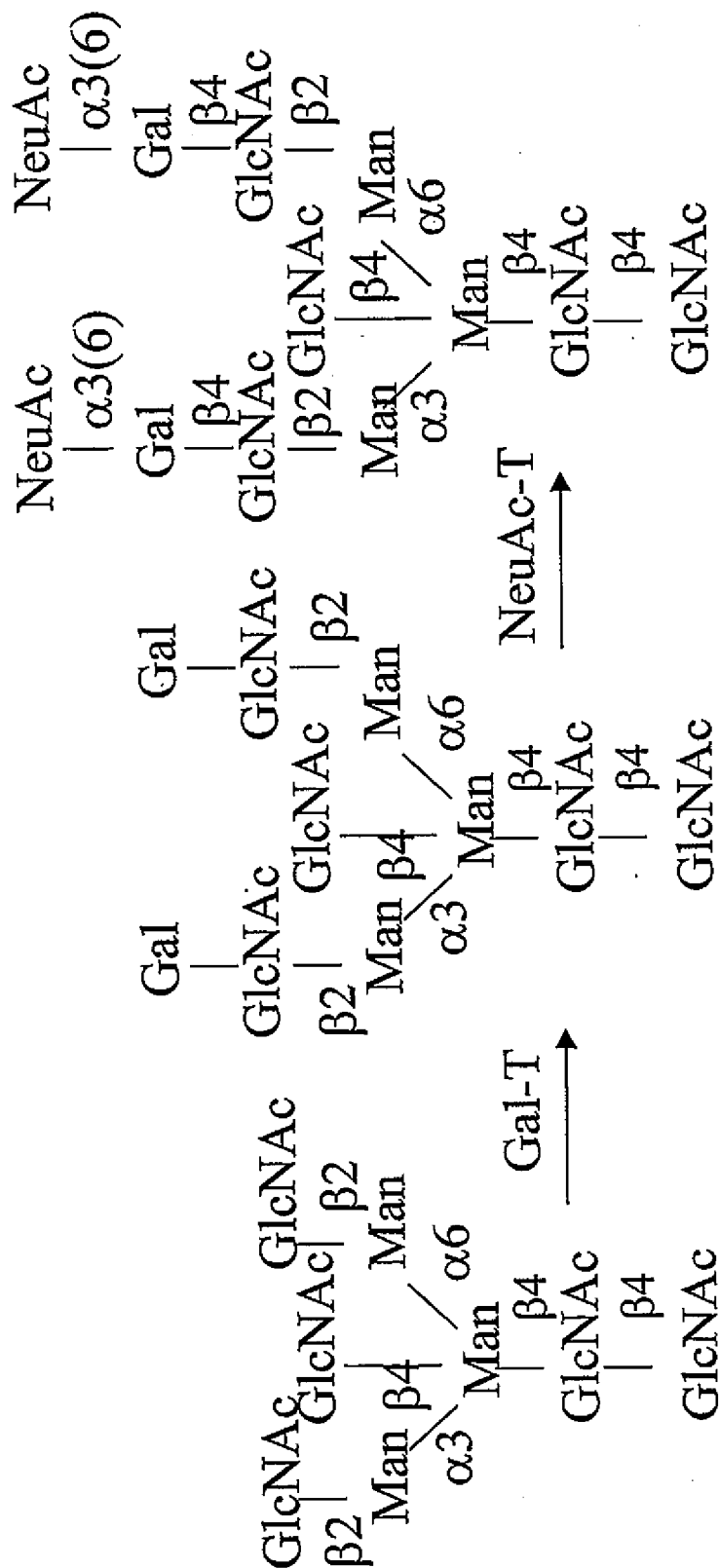


FIG. 4

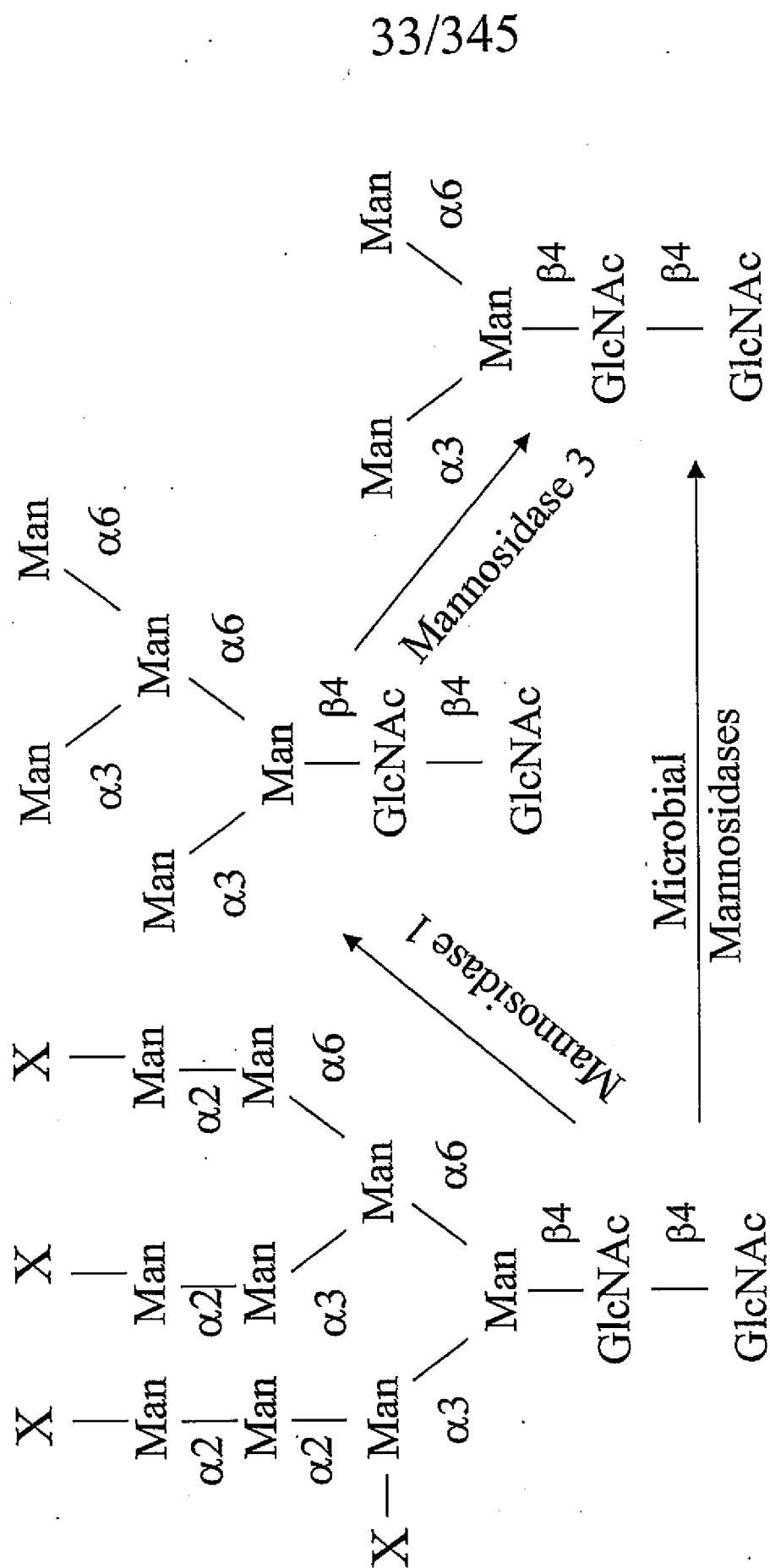


FIG. 5

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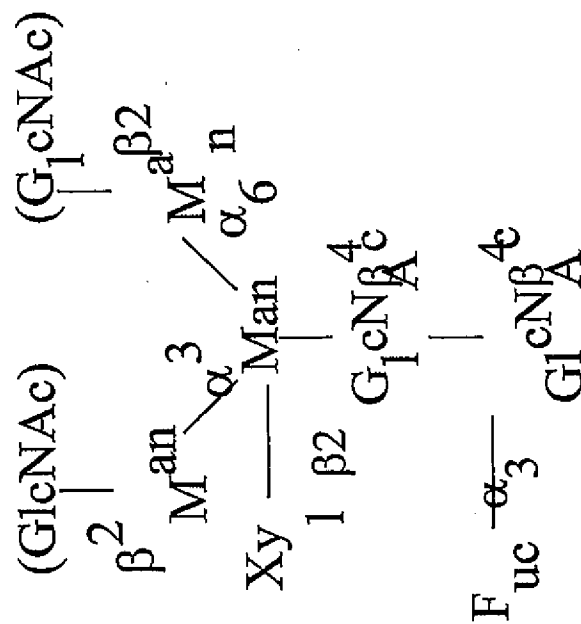


FIG. 6

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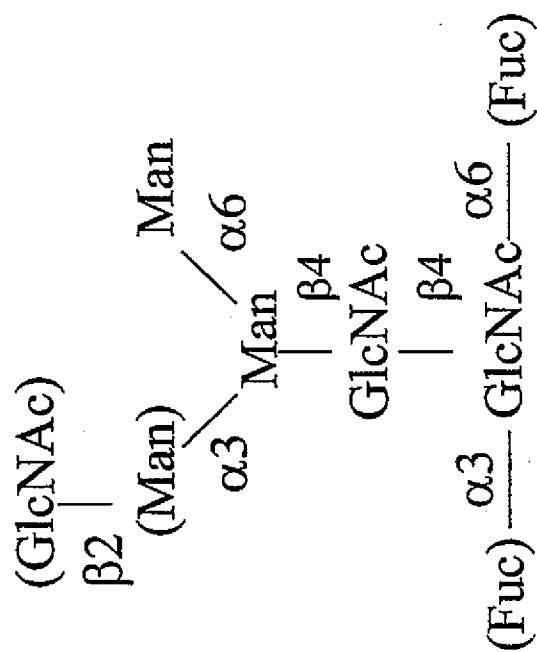


FIG. 7

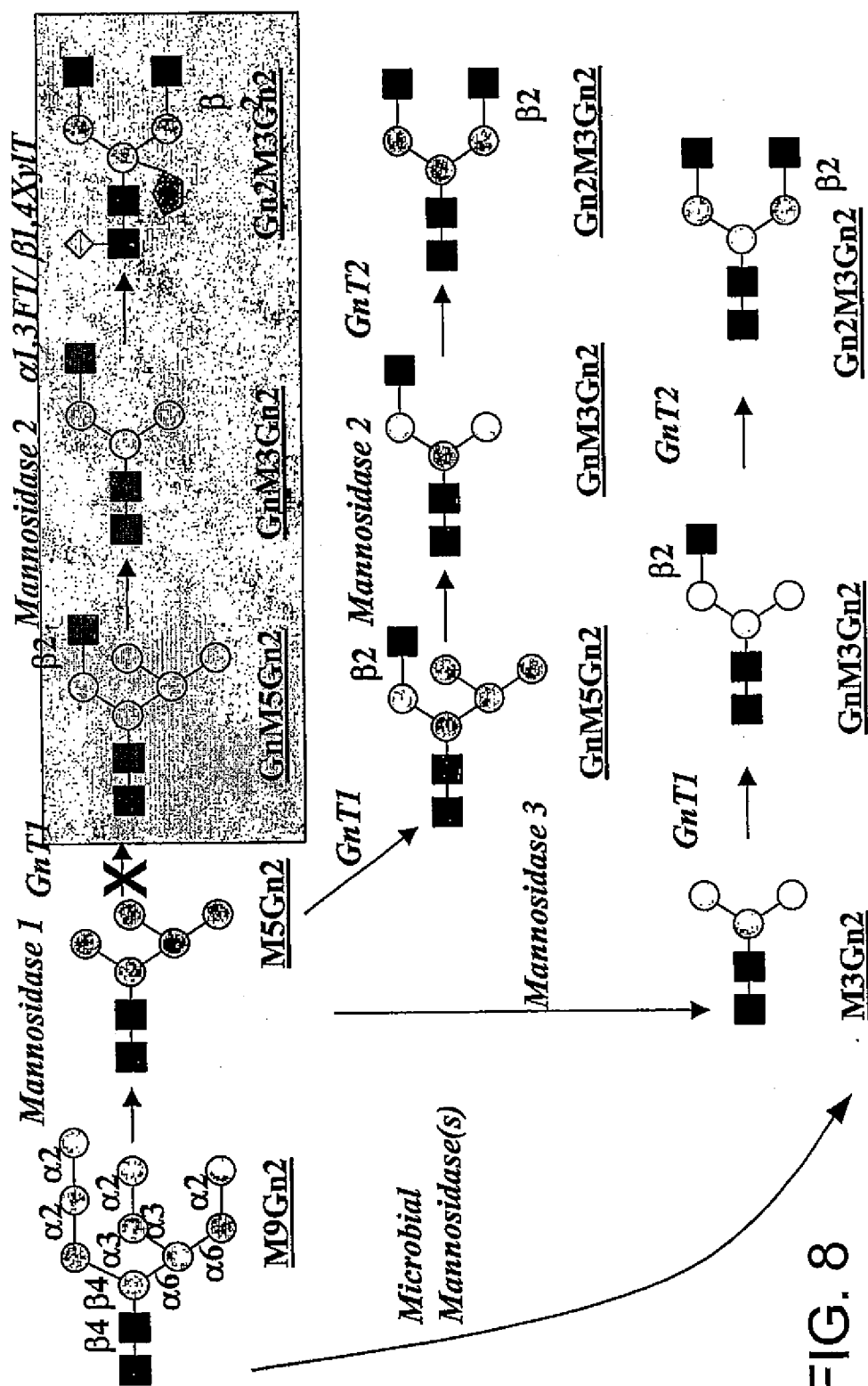


FIG. 8

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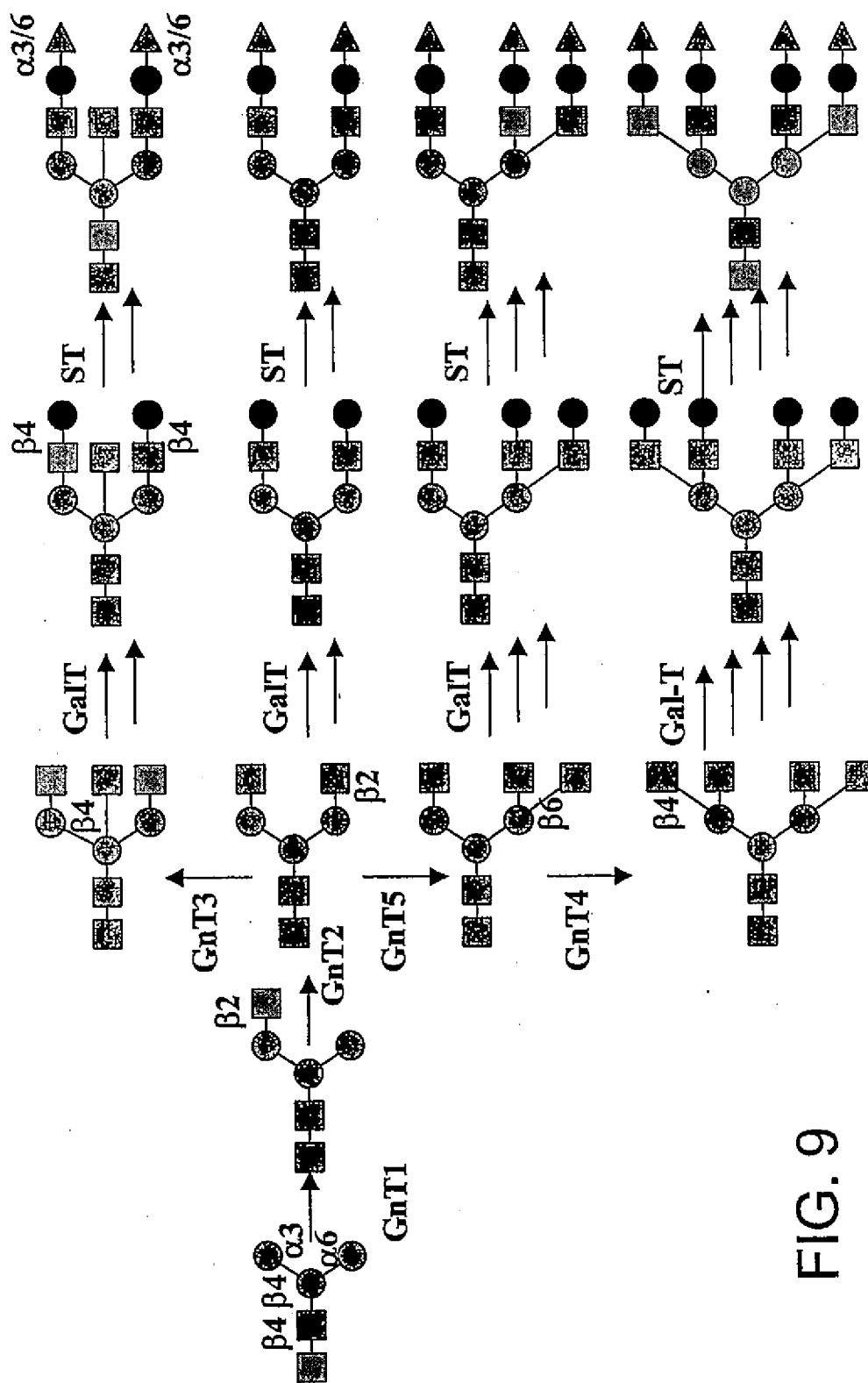


FIG. 9

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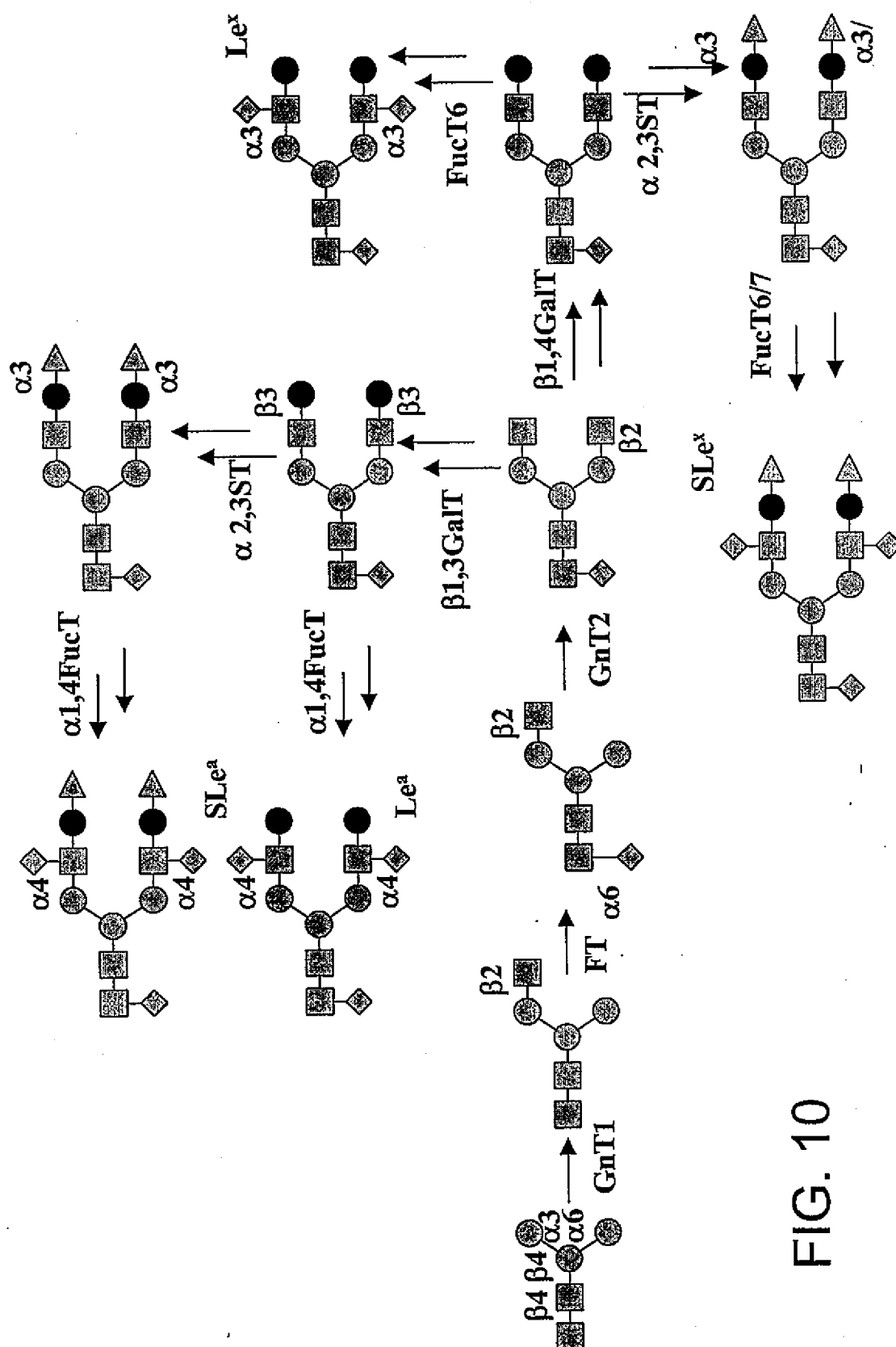


FIG. 10

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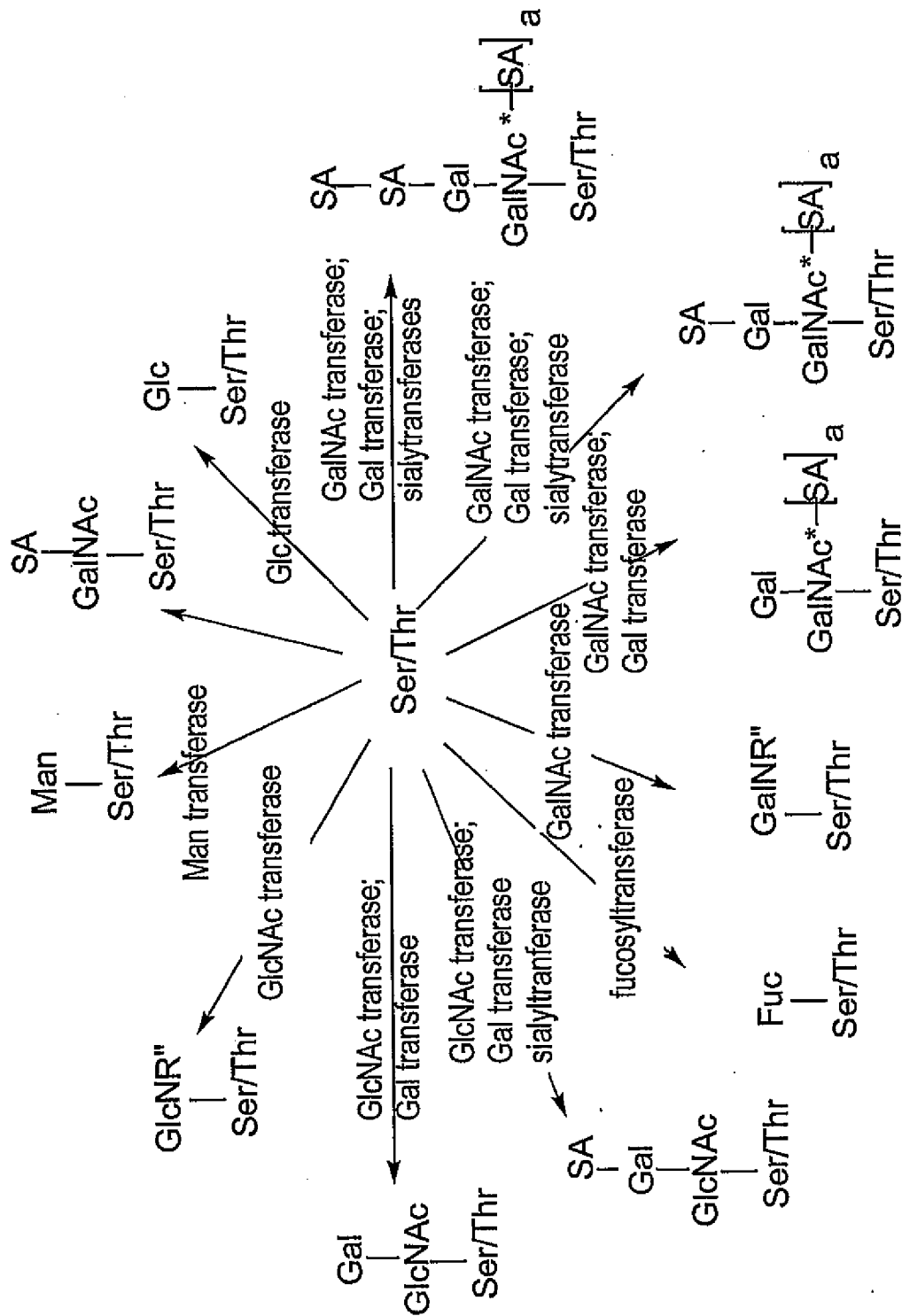


FIG. 11

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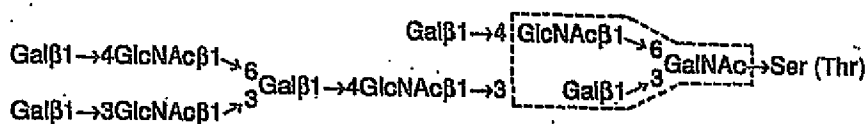
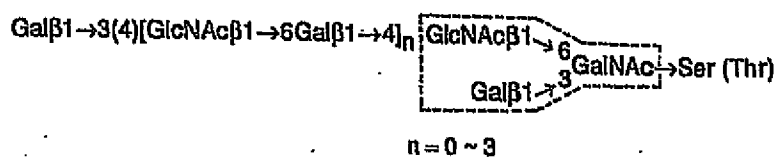
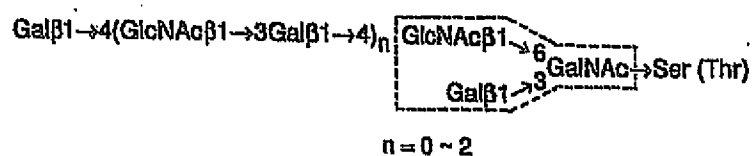
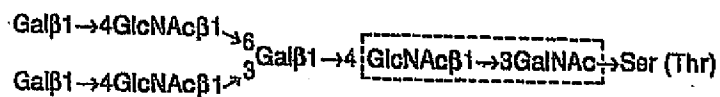
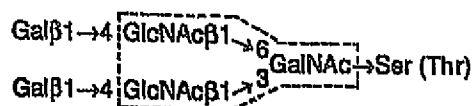
Core 1*Core 2**Core 3**Core 4*

FIG. 12

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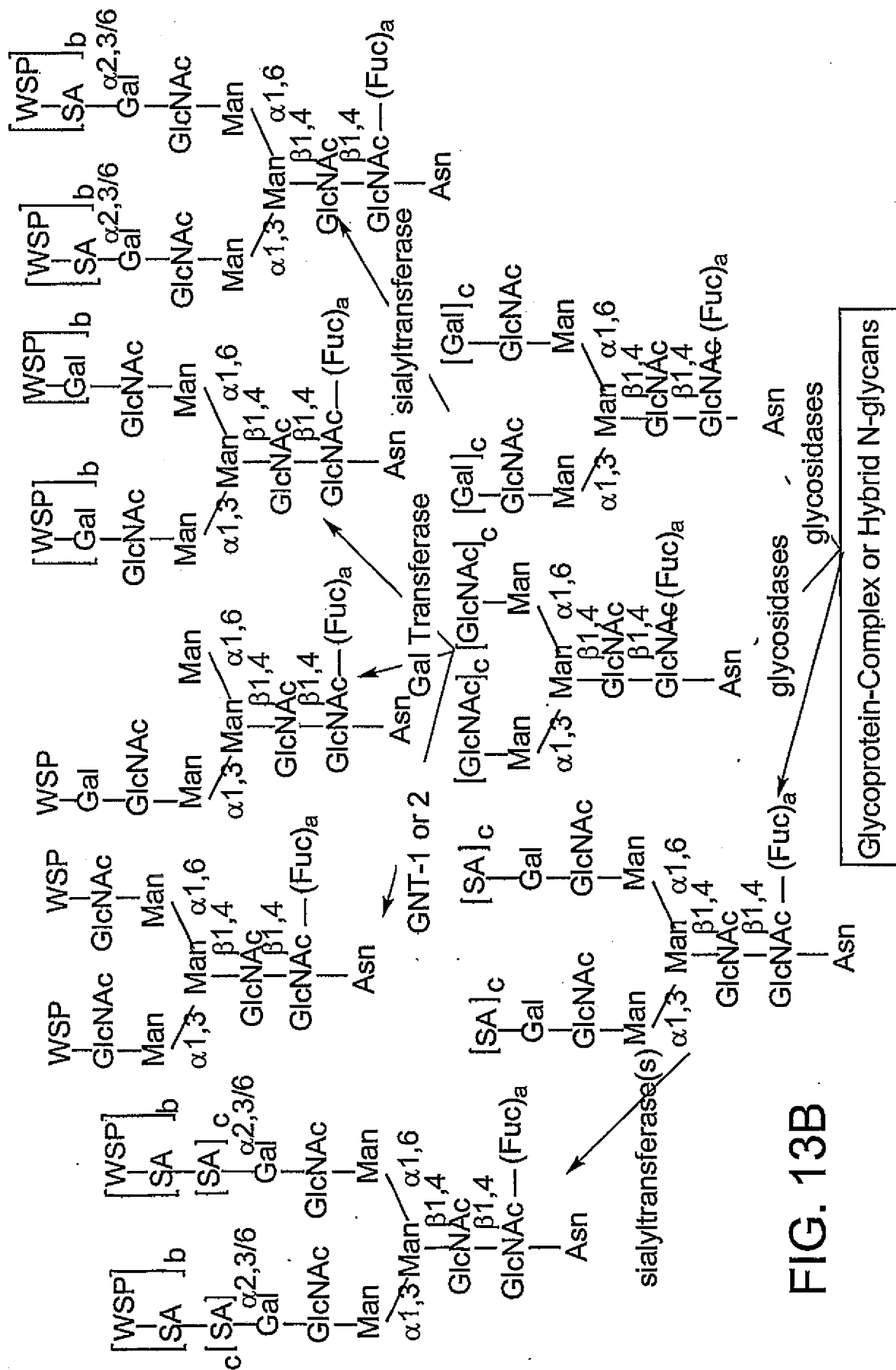


FIG. 13B

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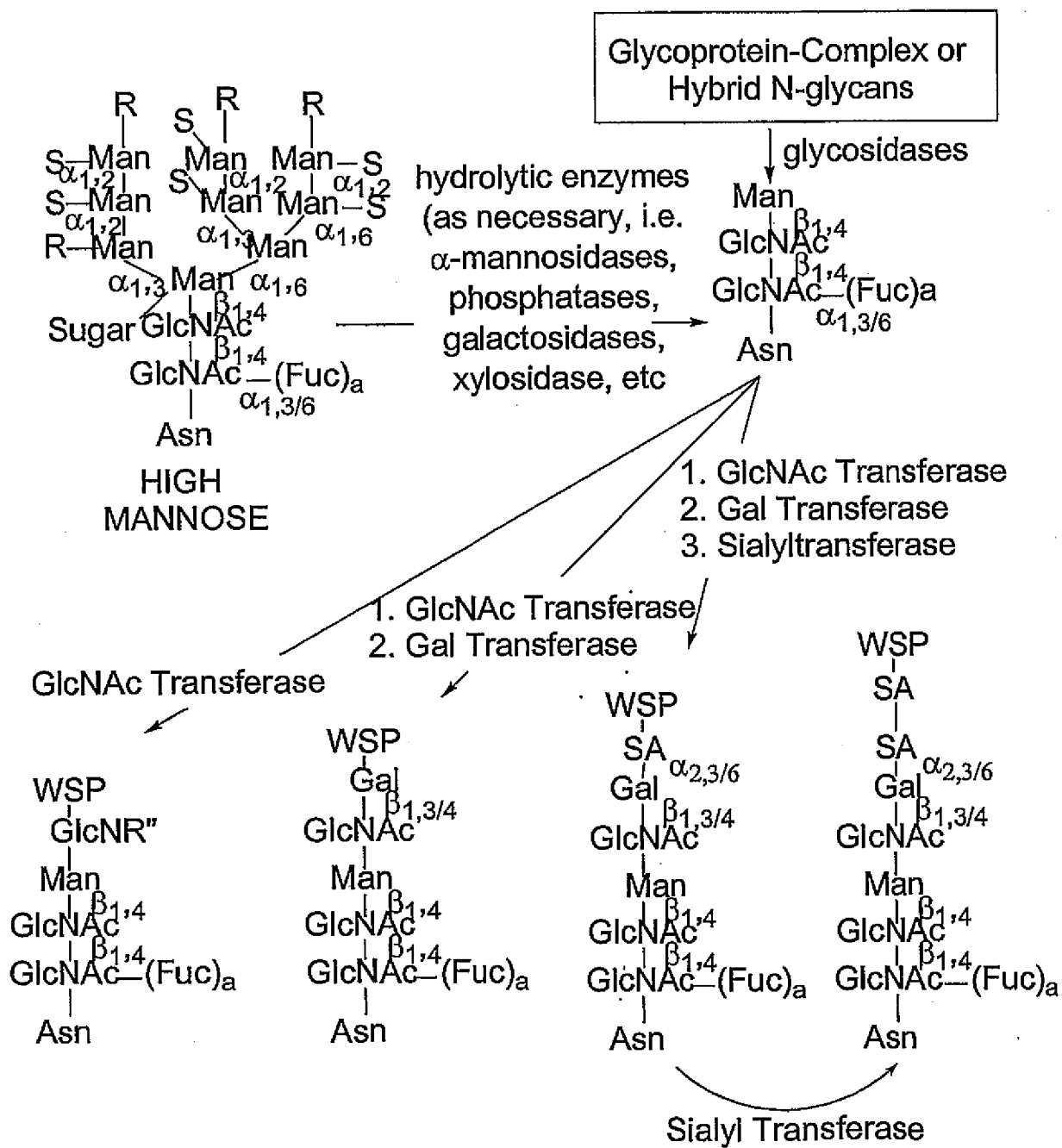


FIG. 14

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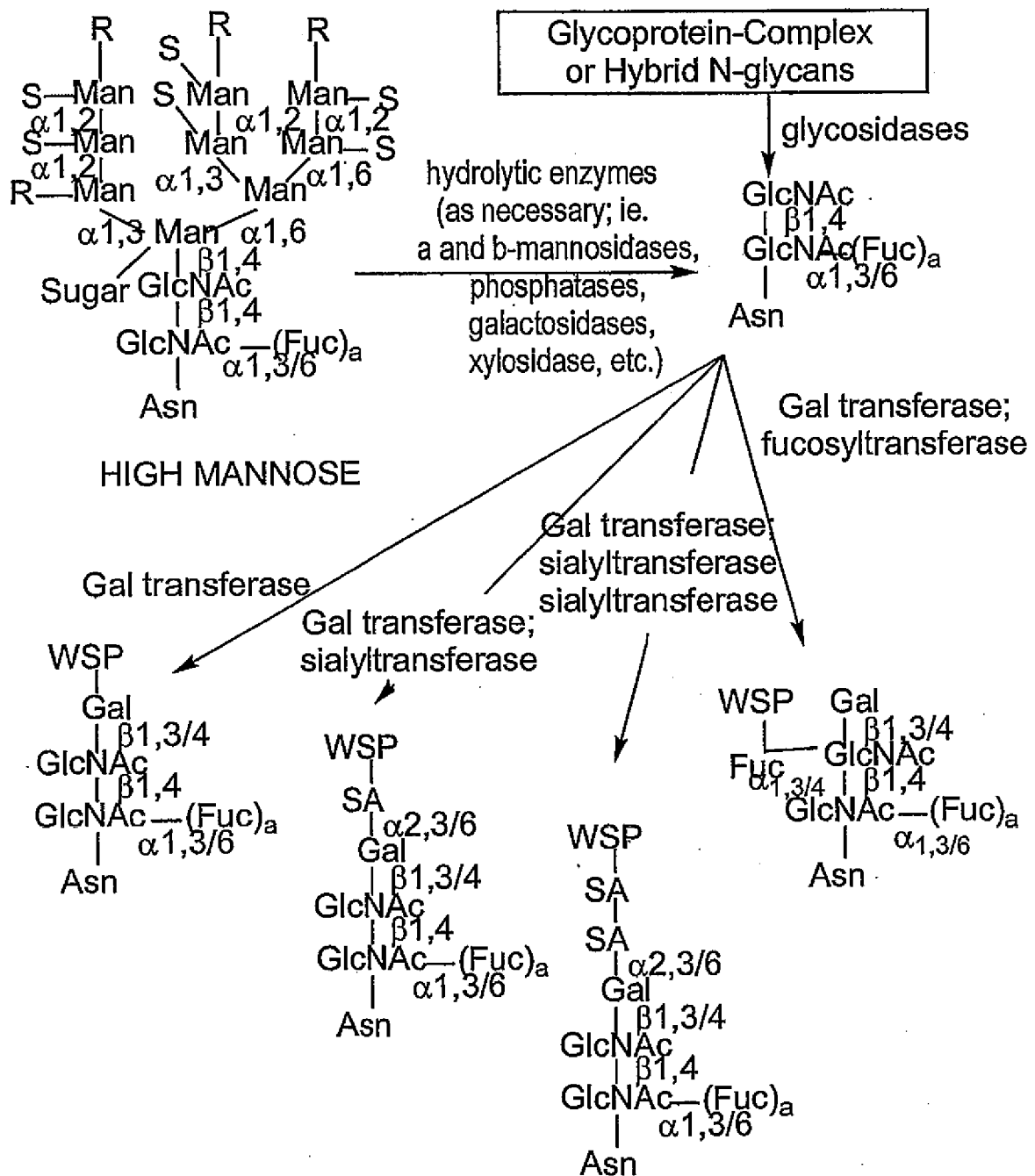


FIG. 15

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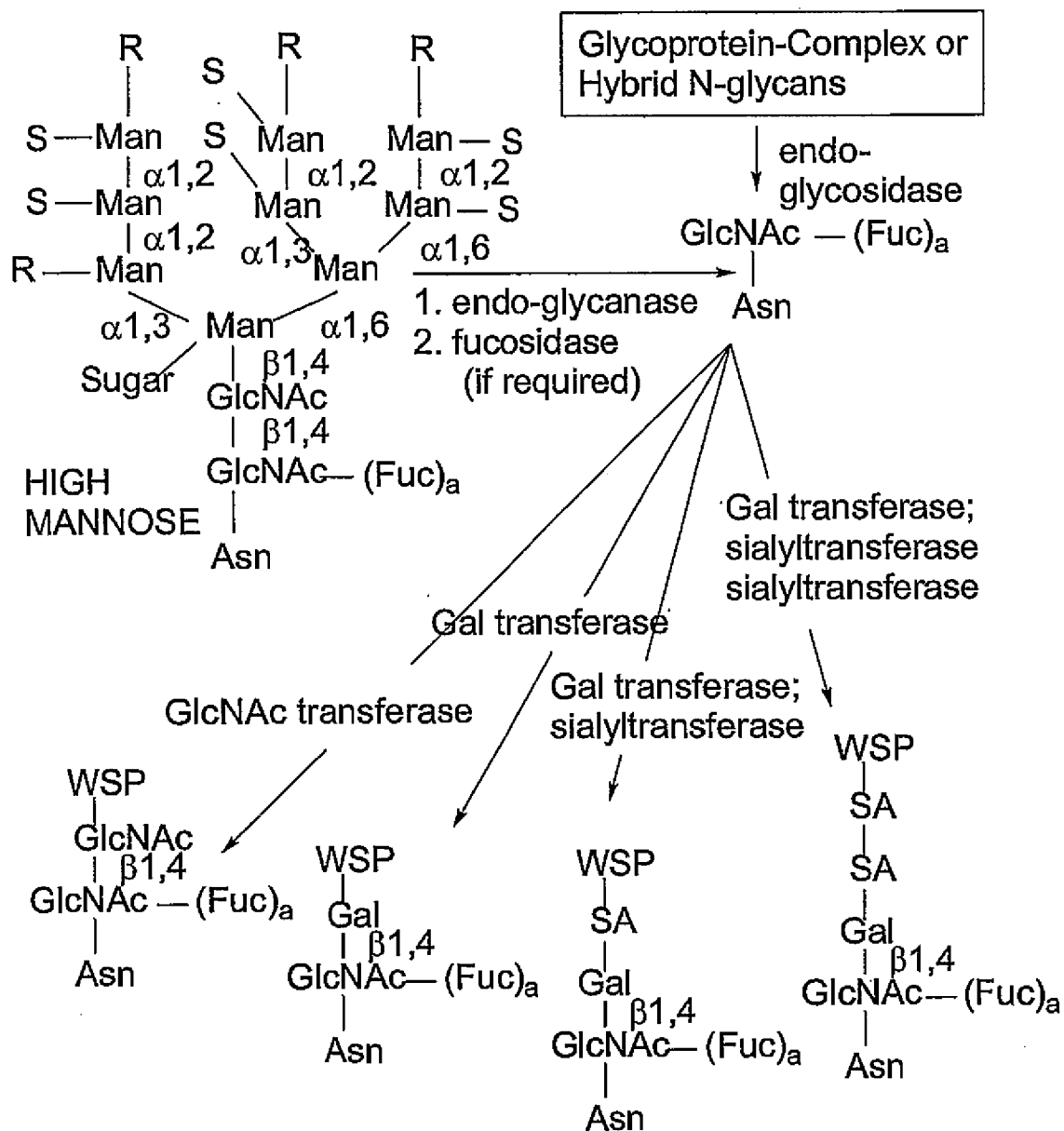


FIG. 16

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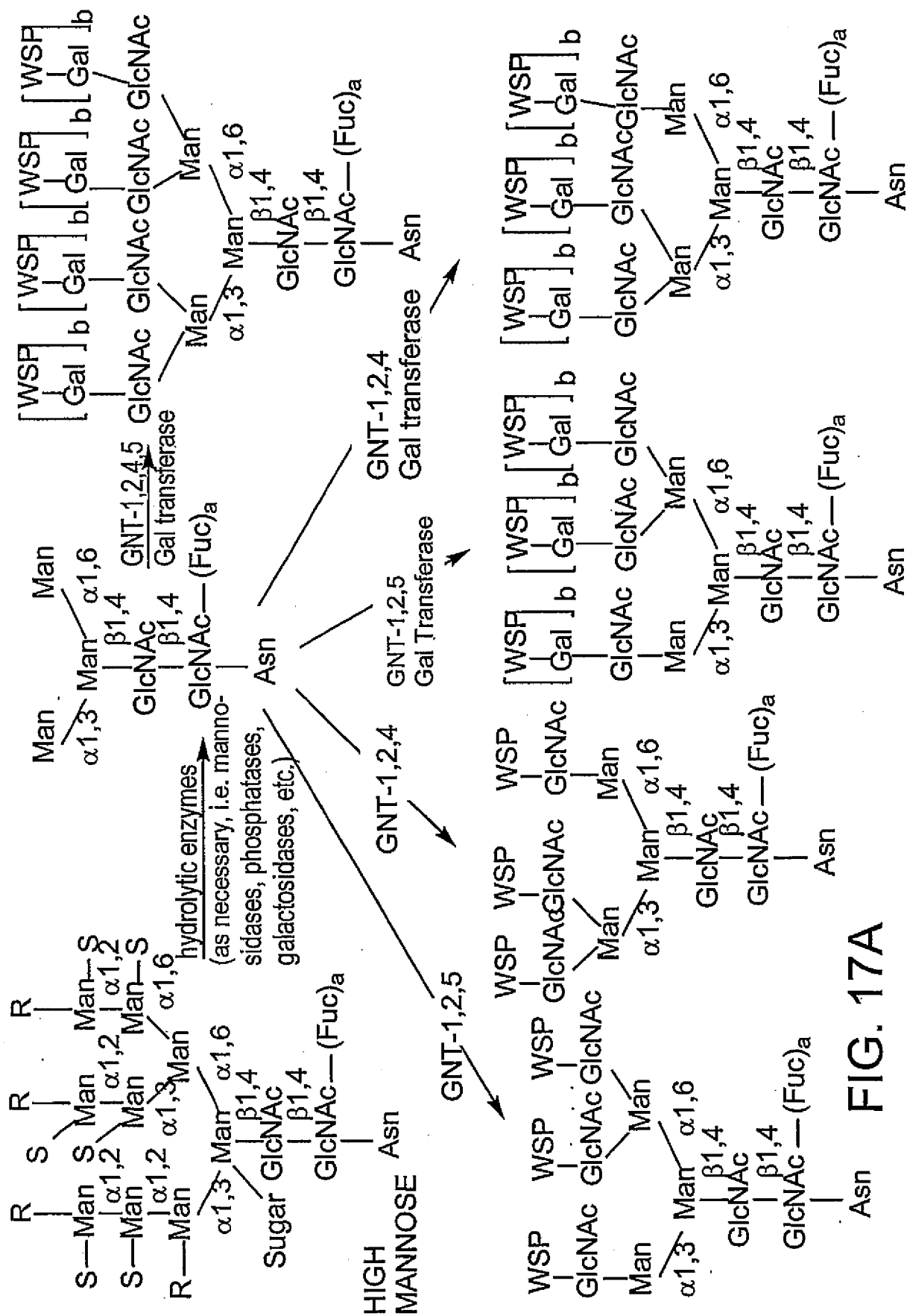
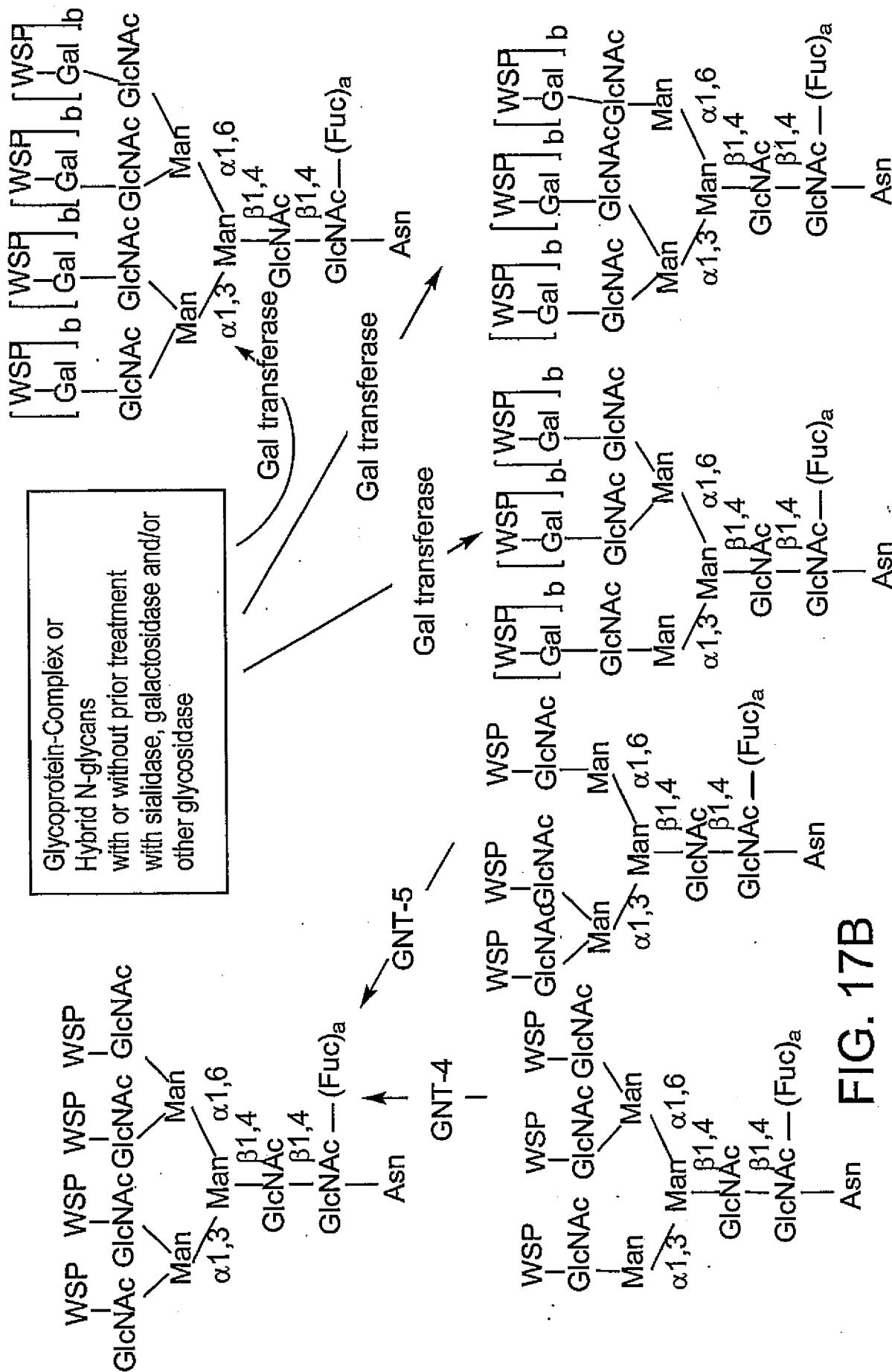
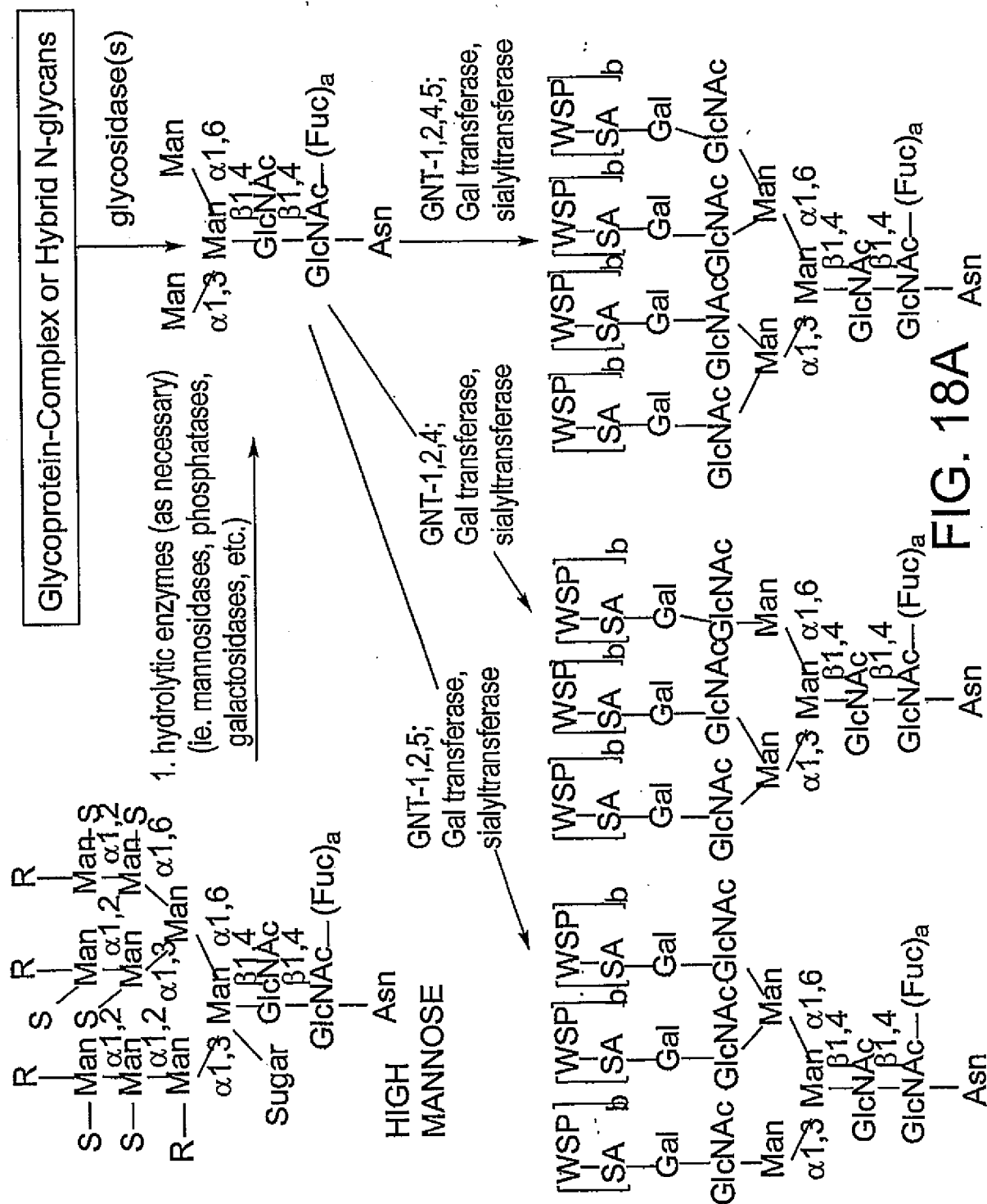


FIG. 17A

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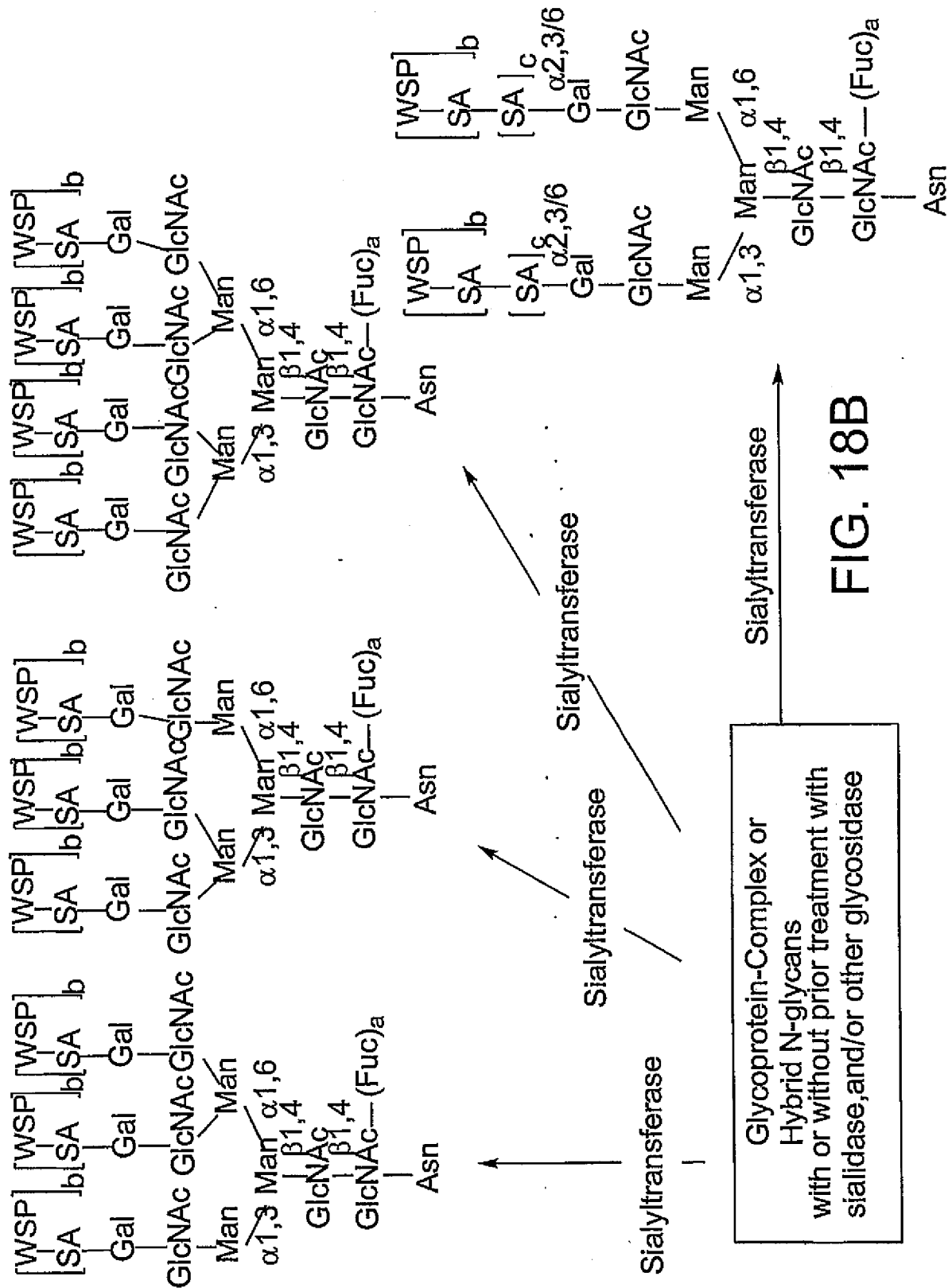


FIG. 18B

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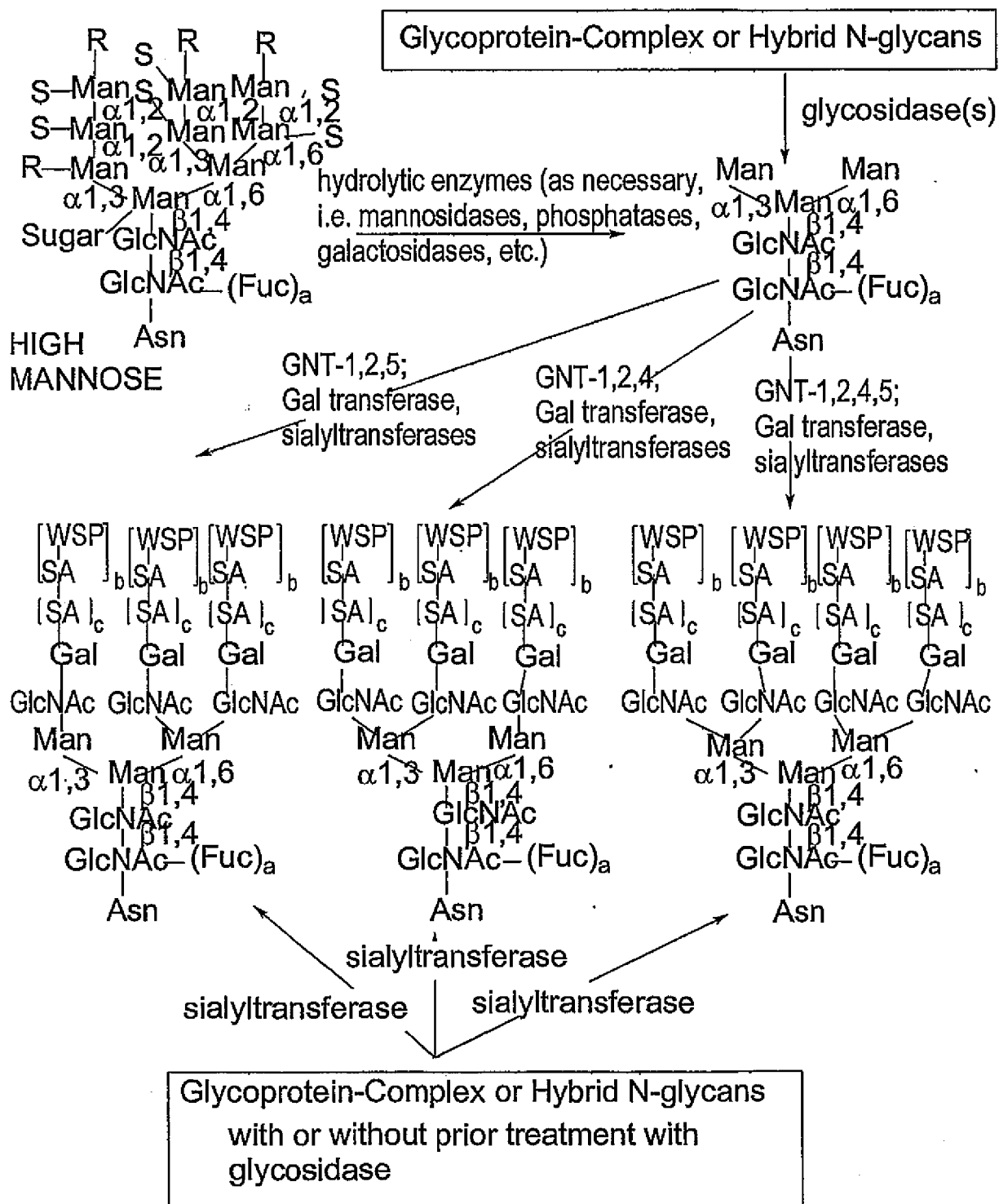


FIG. 19

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O-LINKED OLIGOSACCHARIDES

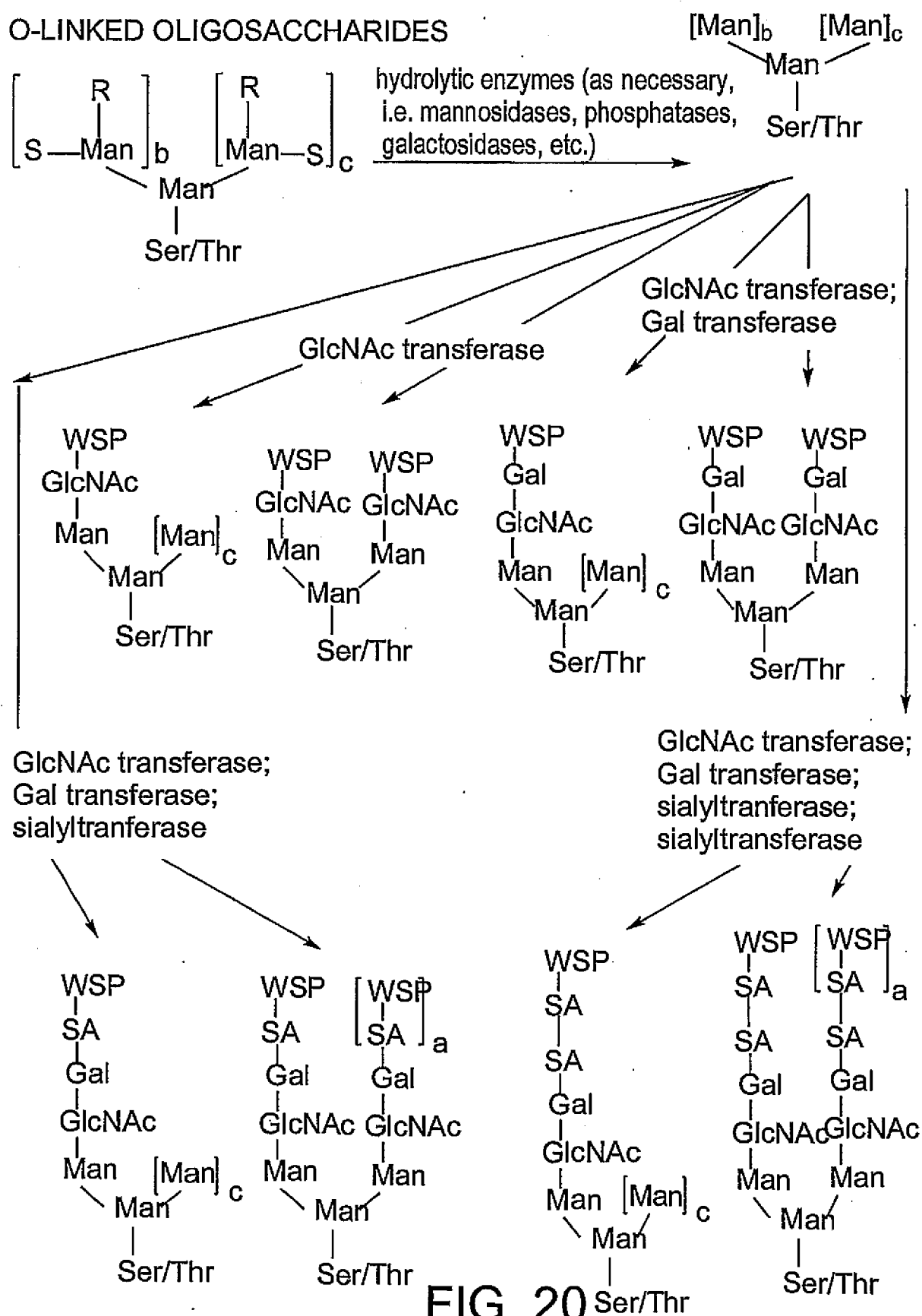


FIG. 20 Ser/Thr

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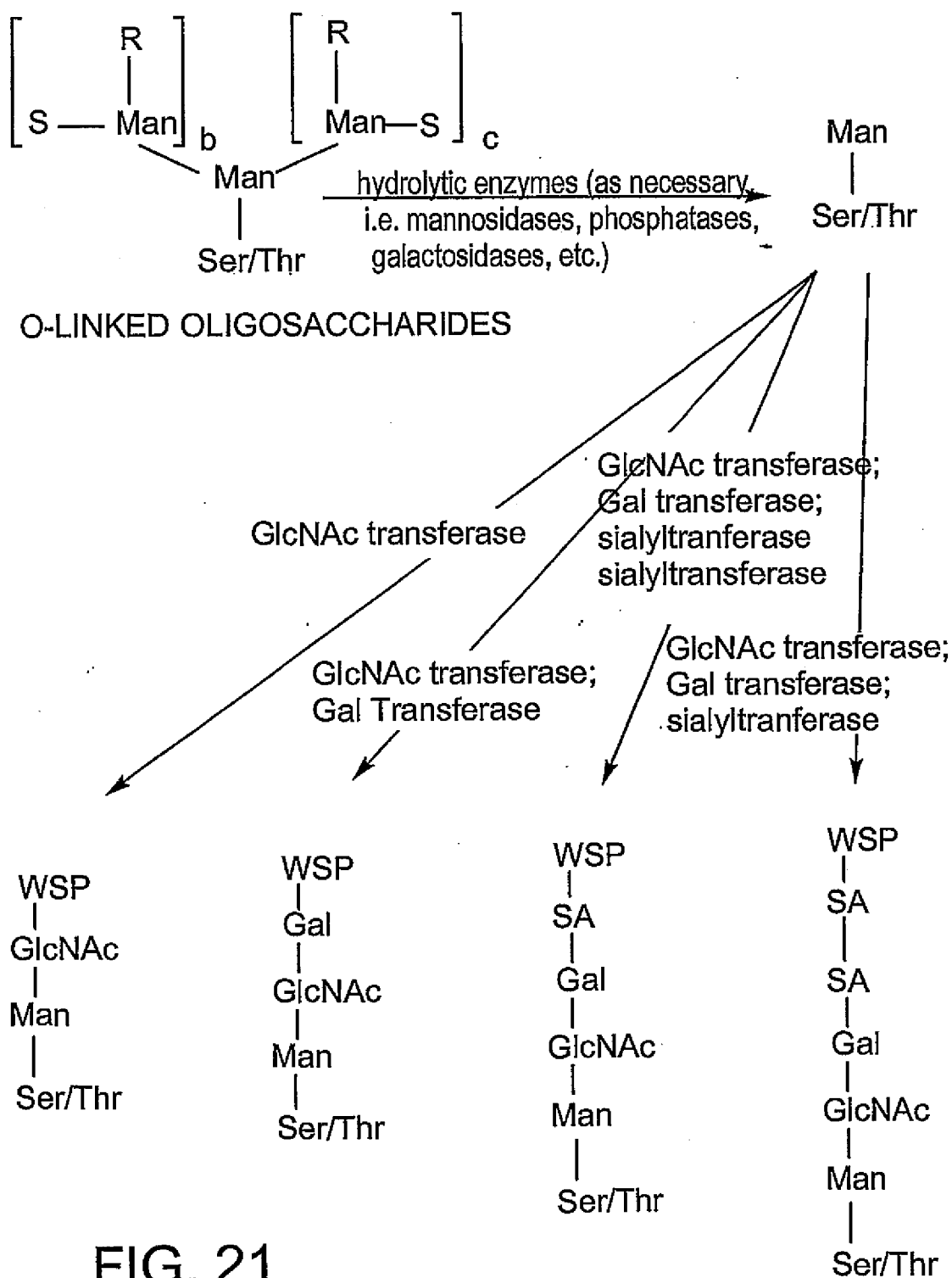


FIG. 21

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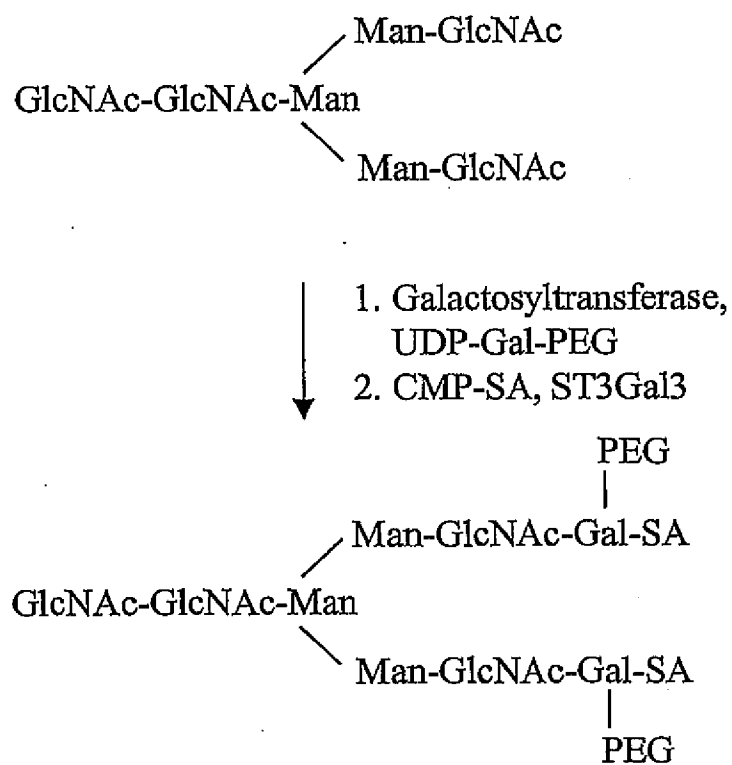


FIG. 22A

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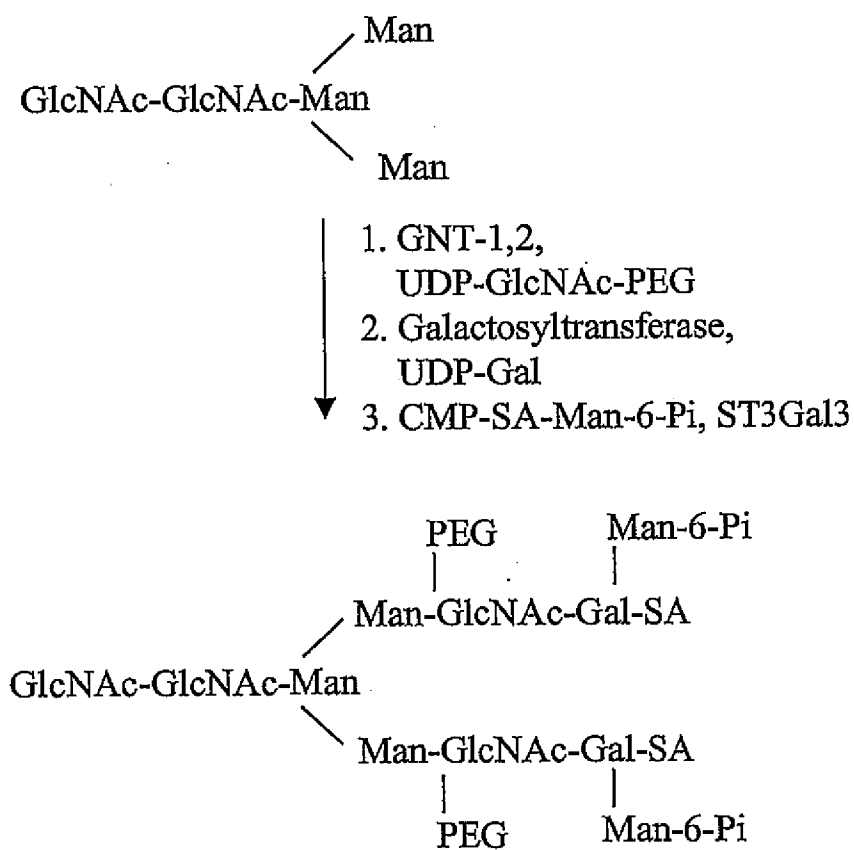


FIG. 22B

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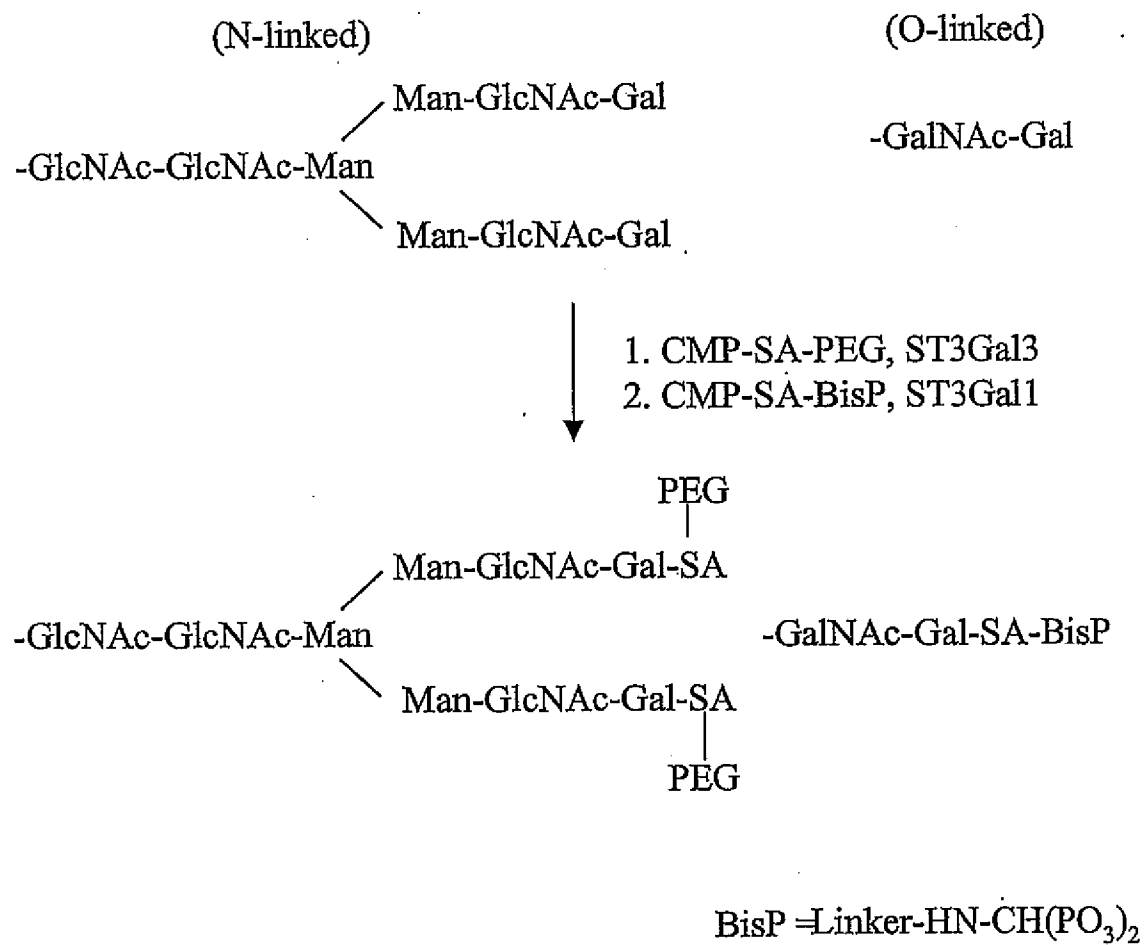


FIG. 22C

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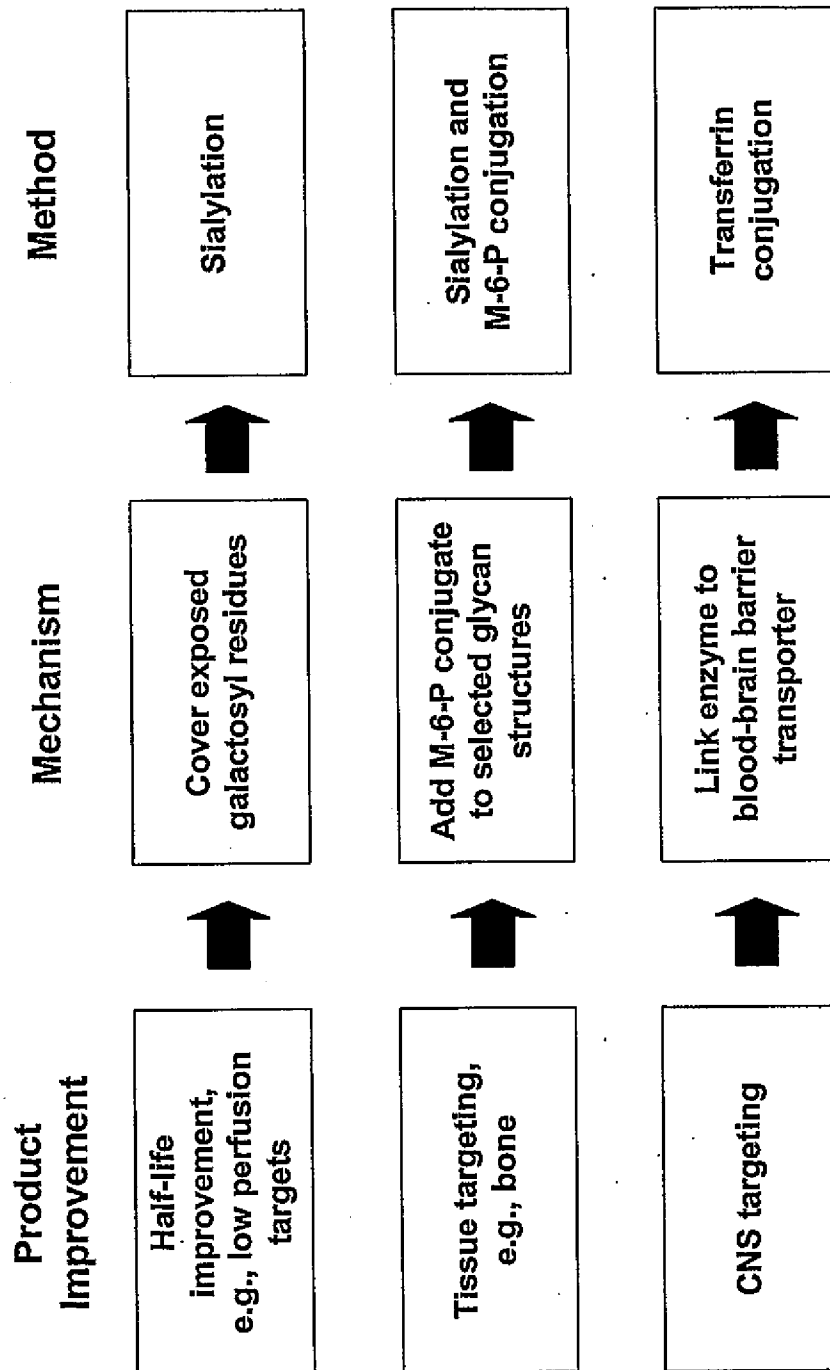


FIG. 23

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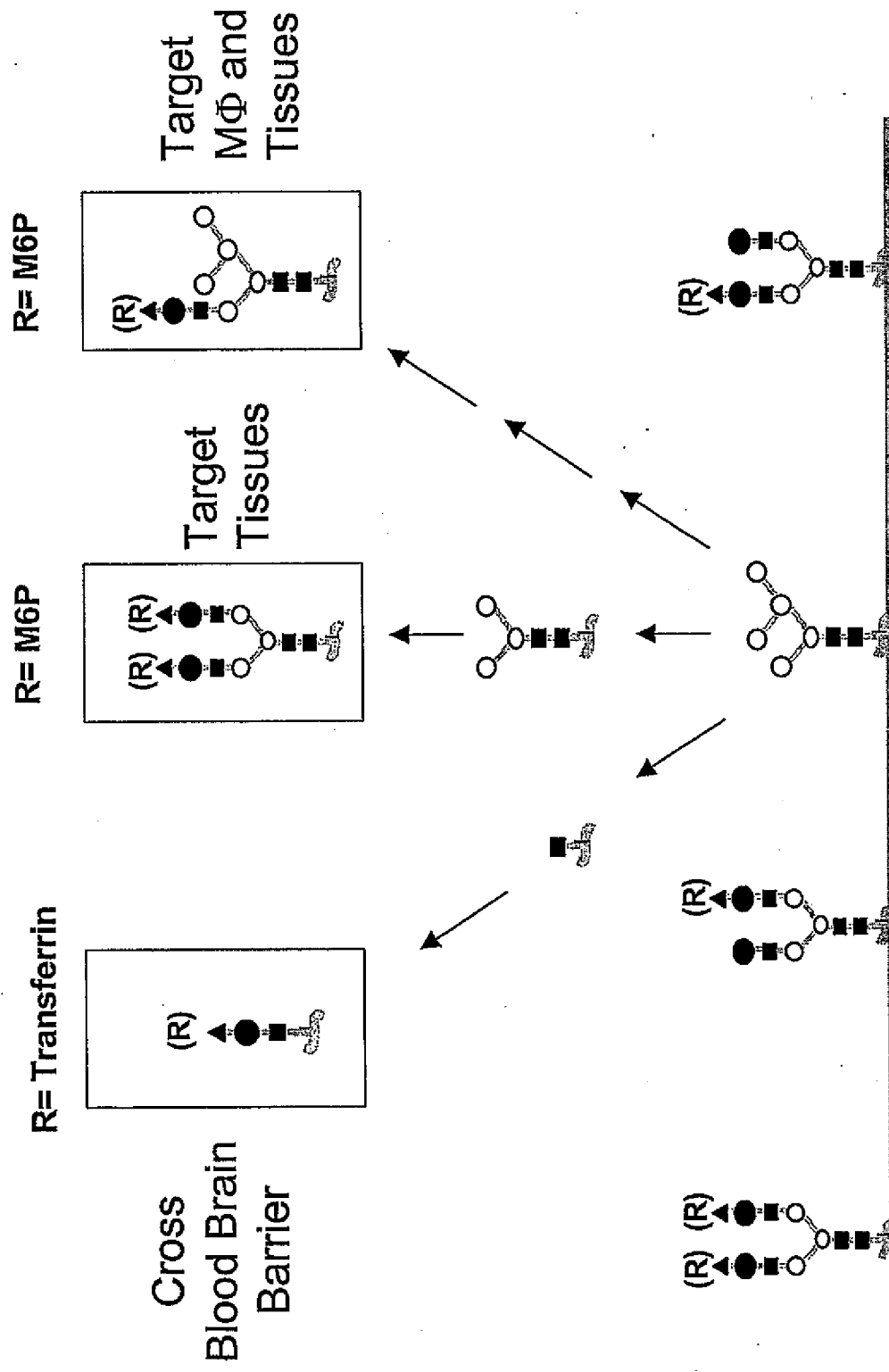


FIG. 24

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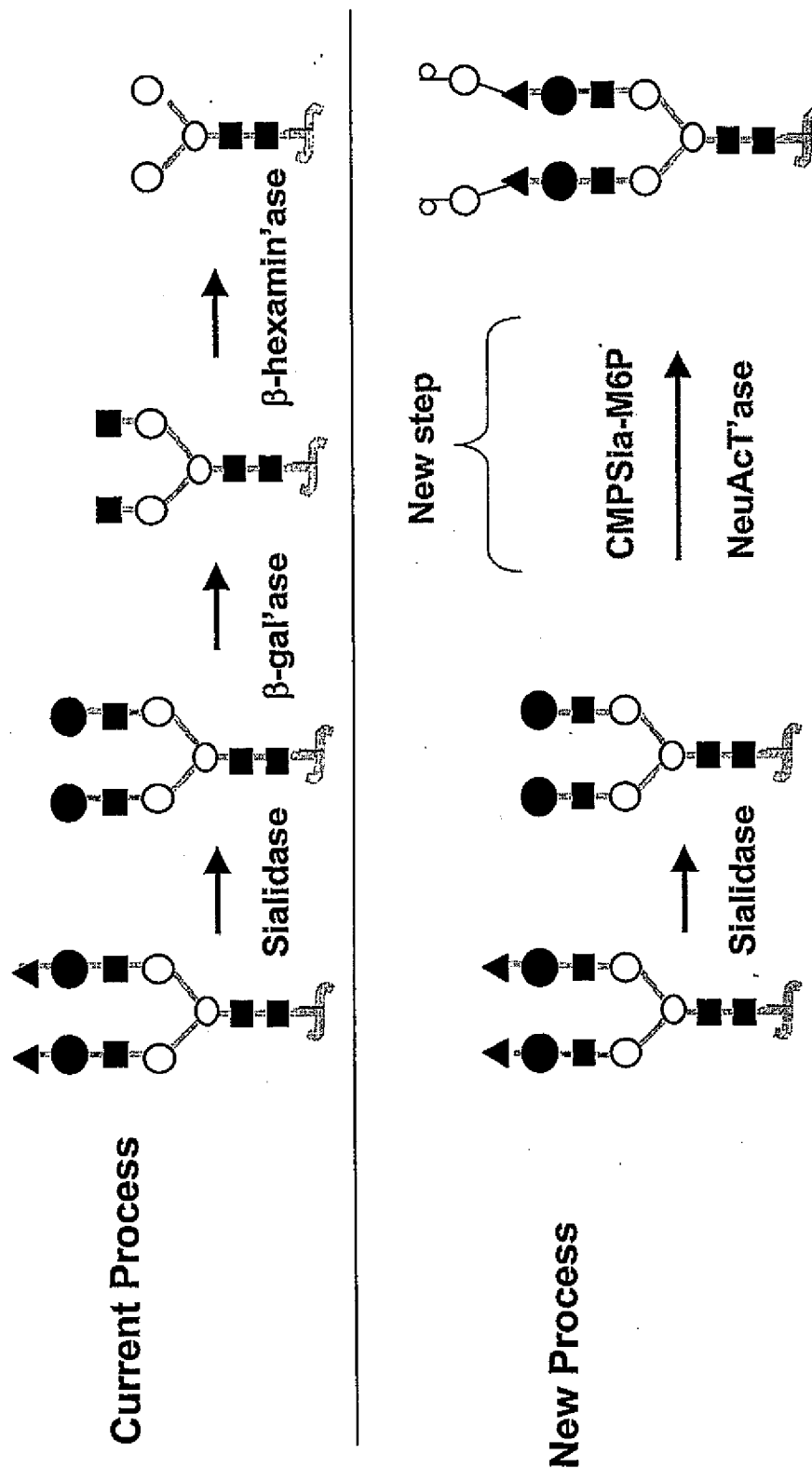


FIG. 25

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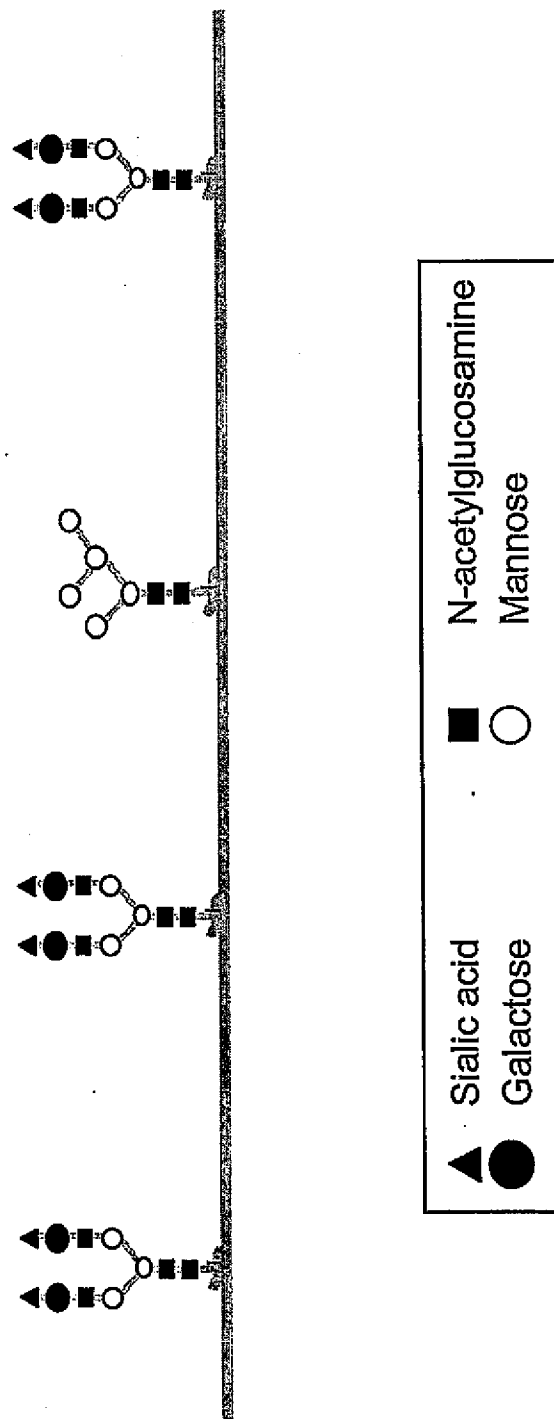
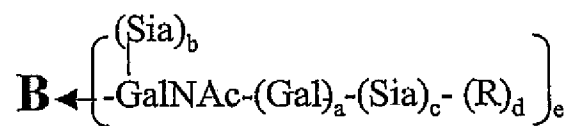
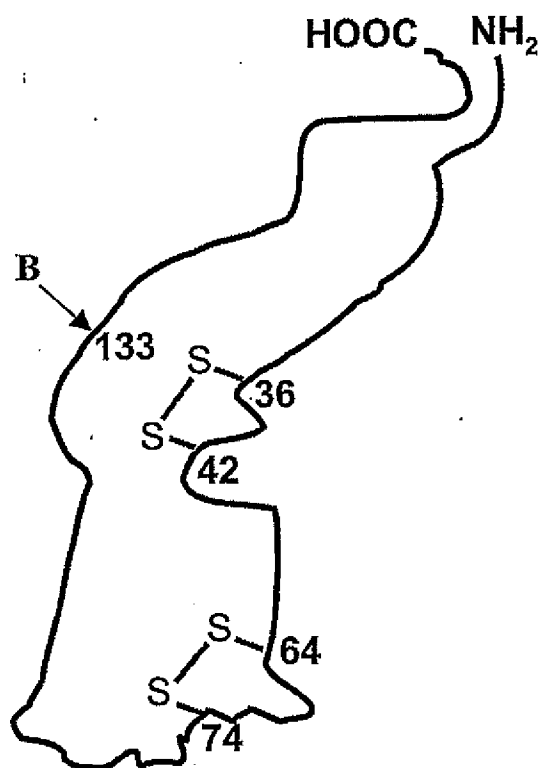


FIG. 26

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose

FIG. 27A

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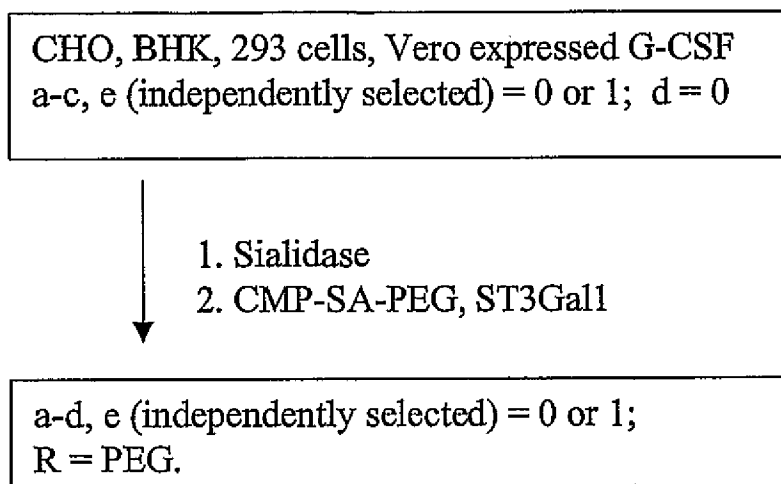


FIG. 27B

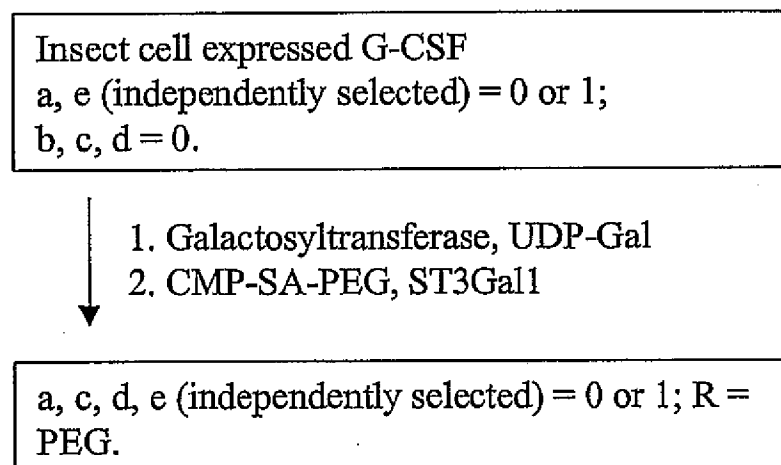


FIG. 27C

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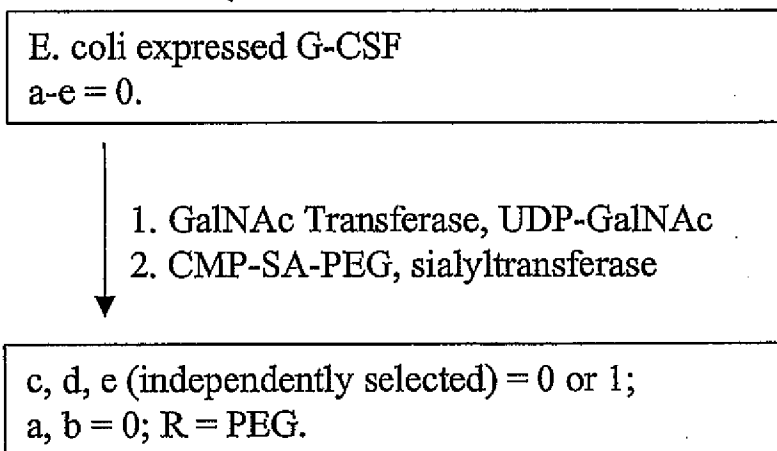


FIG. 27D

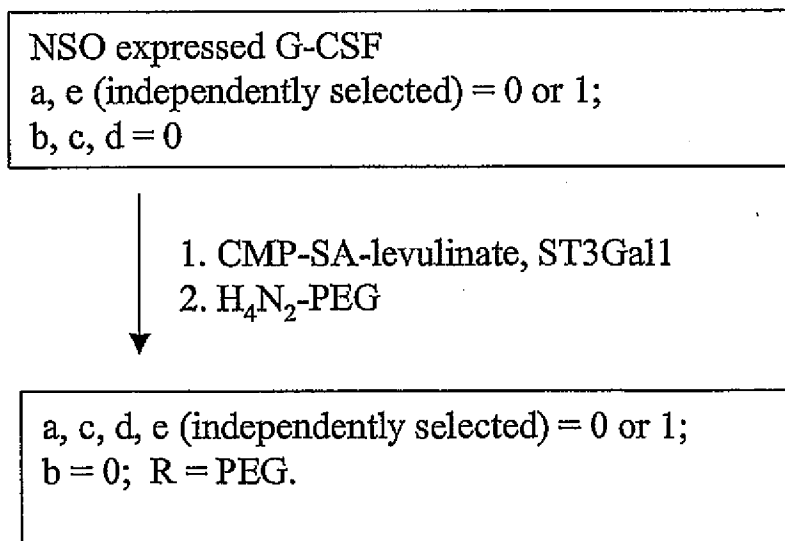


FIG. 27E

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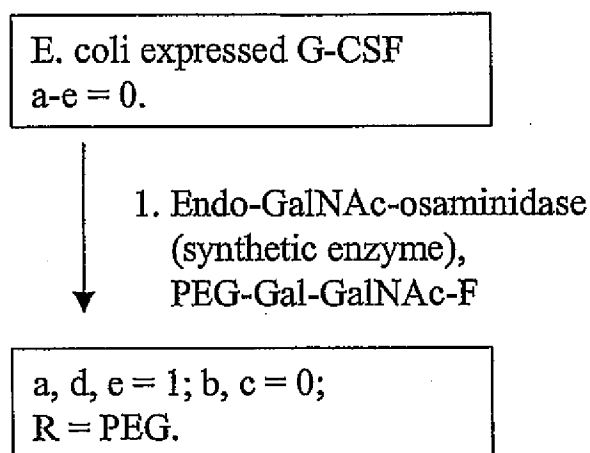


FIG. 27F

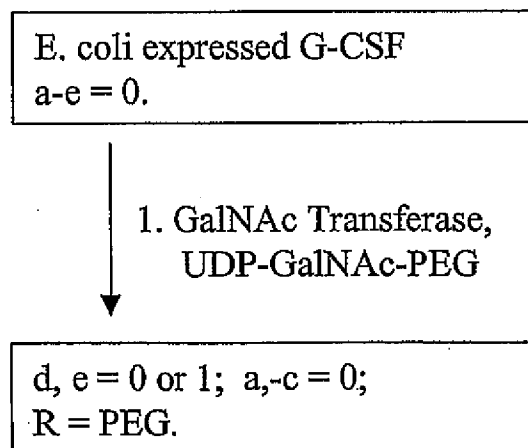
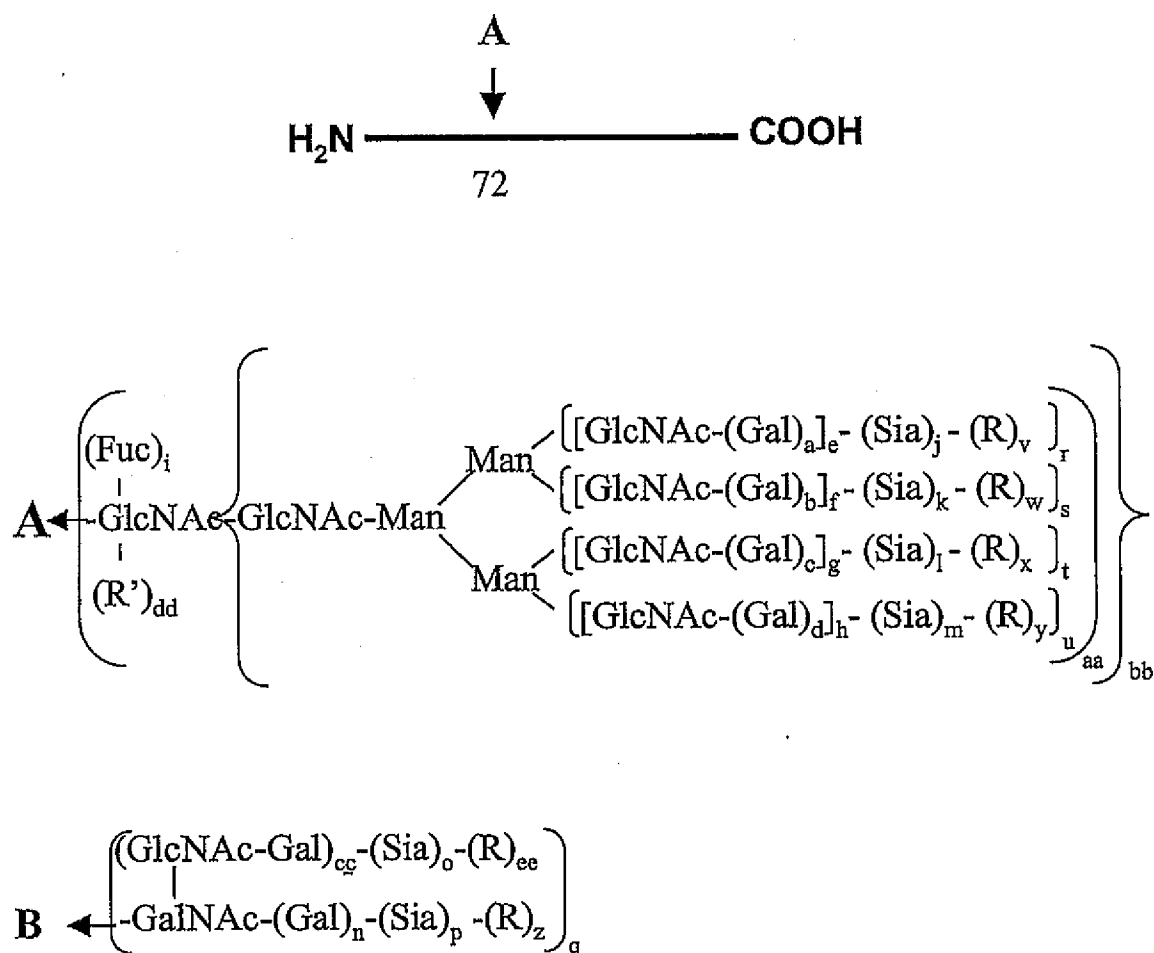


FIG. 27G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 28A

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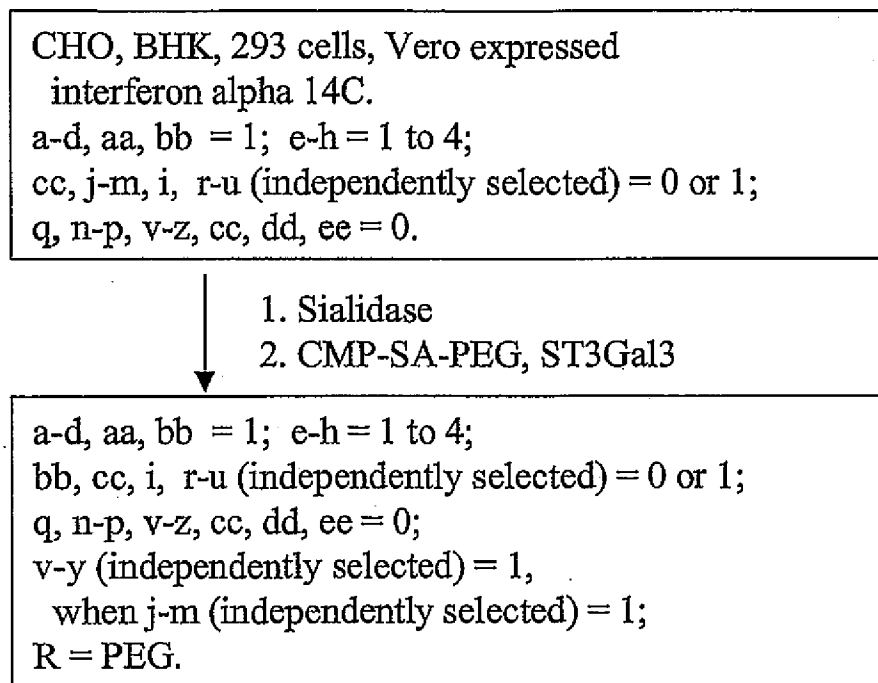


FIG. 28B

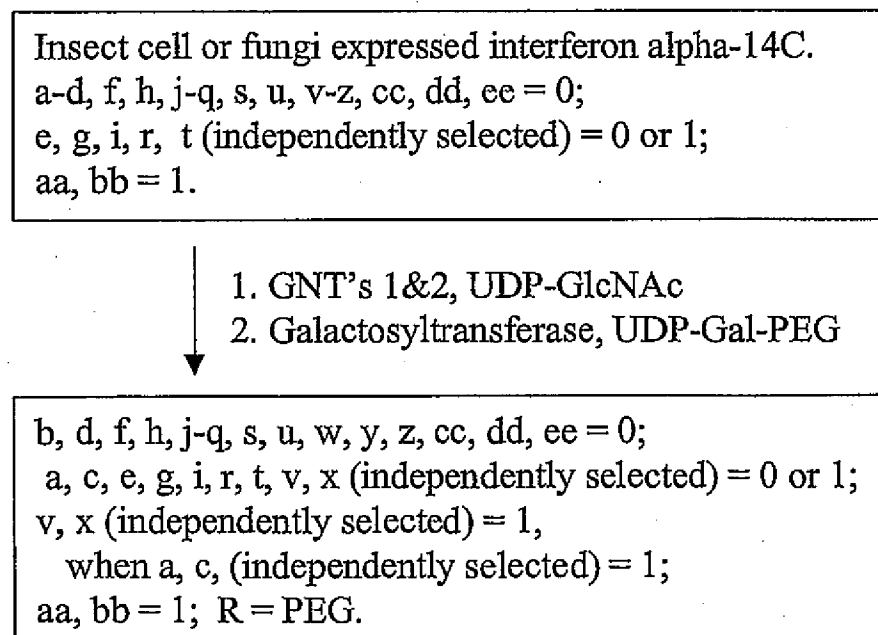


FIG. 28C

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Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

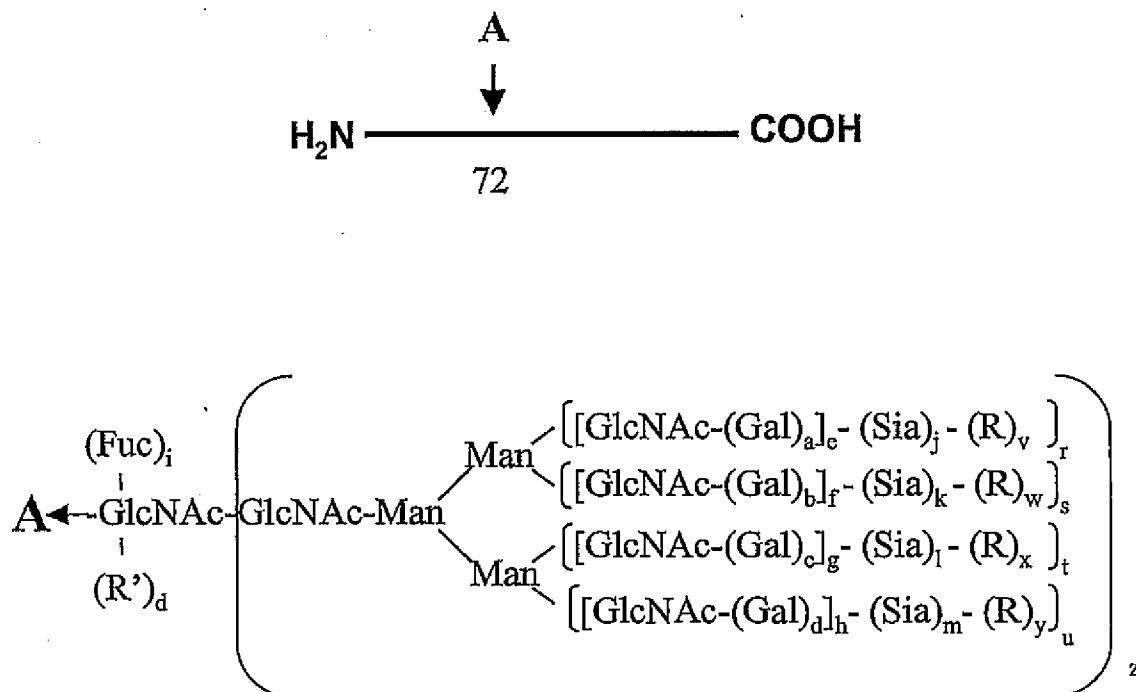
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 28D

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 28E

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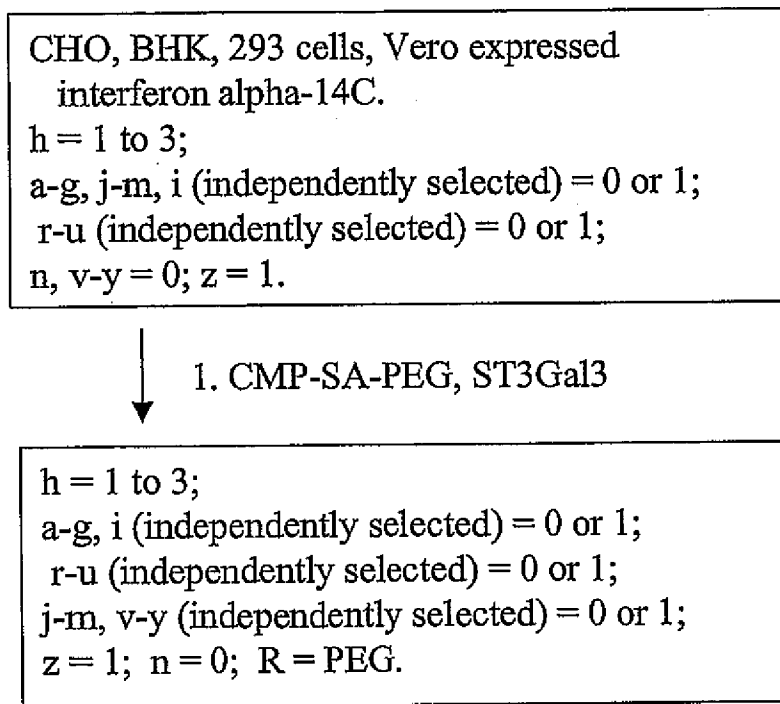


FIG. 28F

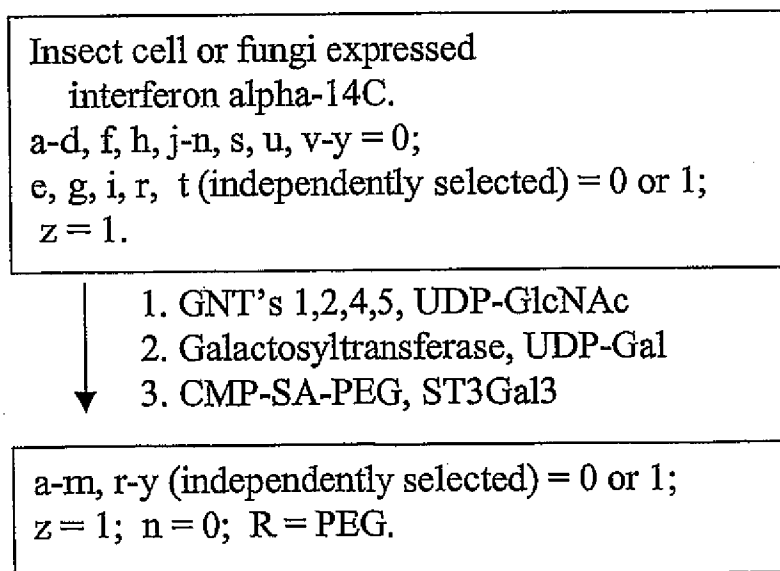


FIG. 28G

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Yeast expressed interferon alpha-14C.
 $a-n = 0$; $r-y$ (independently selected) = 0 to 1;
 $z = 1$; R (branched or linear) = Man,
 oligomannose.

- ↓
1. mannosidases
 2. GNT's 1,2,4,5, UDP-GlcNAc
 3. Galactosyltransferase, UDP-Gal
 4. CMP-SA-PEG, ST3Gal3

$a-m, r-y$ (independently selected) = 0 or 1;
 $z = 1$; $n = 0$; $R = \text{PEG}$.

FIG. 28H

NSO expressed interferon alpha 14C.
 $a-i, r-u$ (independently selected) = 0 or 1;
 $j-m, n, v-y = 0$; $z = 1$.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

$a-i, j-m, r-y$ (independently selected) = 0 or 1;
 $n = 0$; $z = 1$; $R = \text{PEG}$.

FIG. 28I

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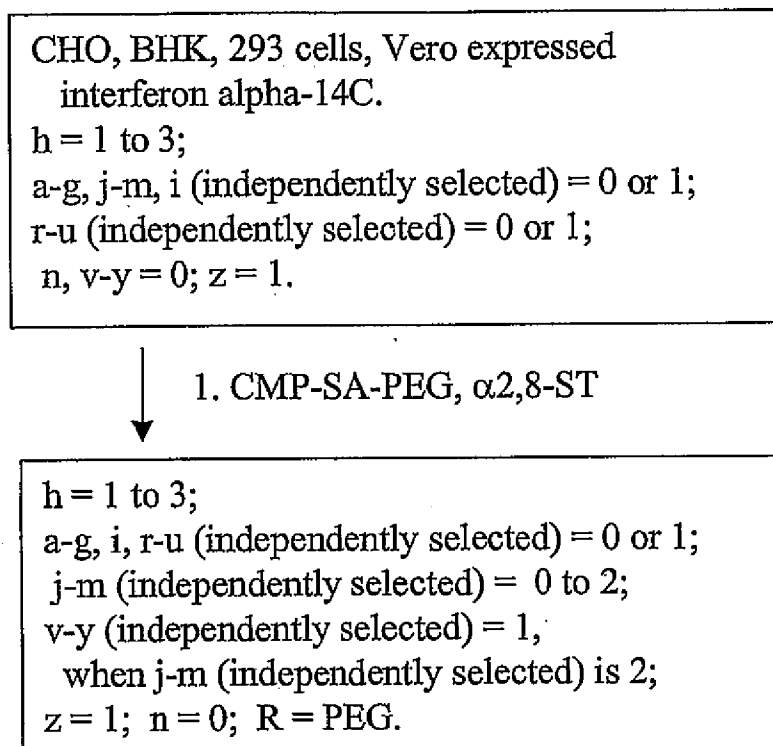


FIG. 28J

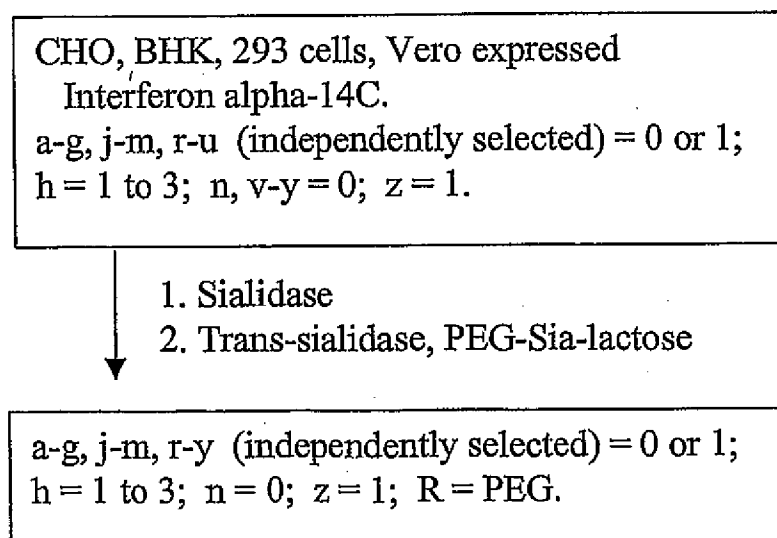


FIG. 28K

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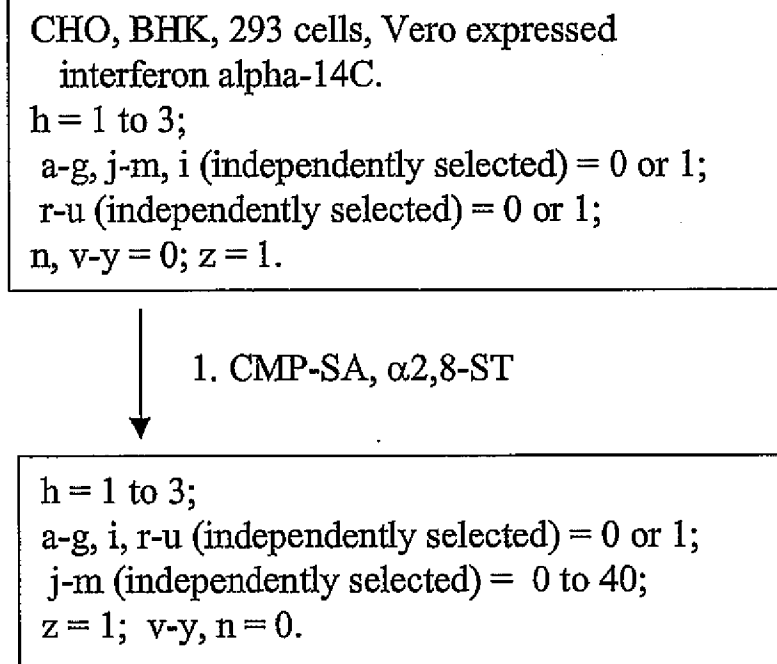


FIG. 28L

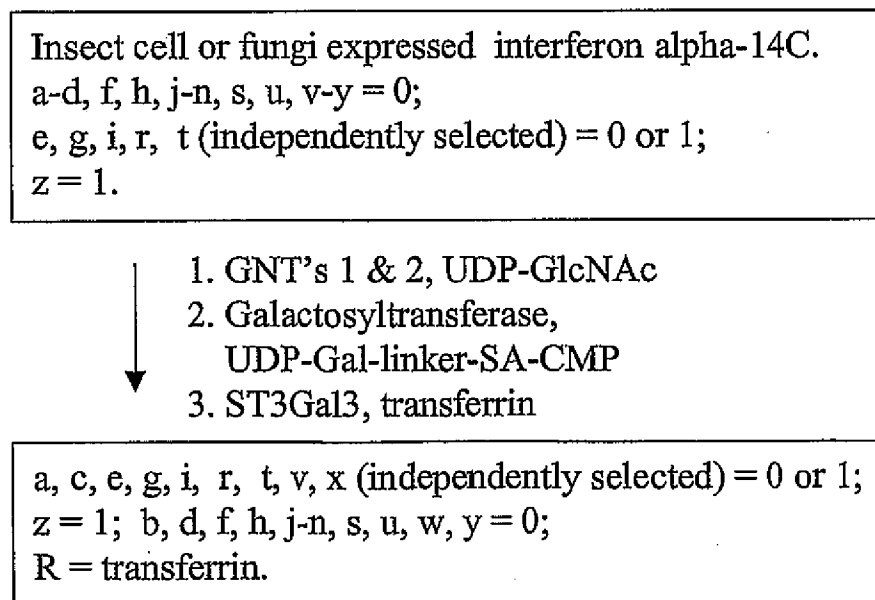


FIG. 28M

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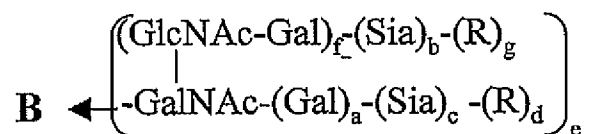
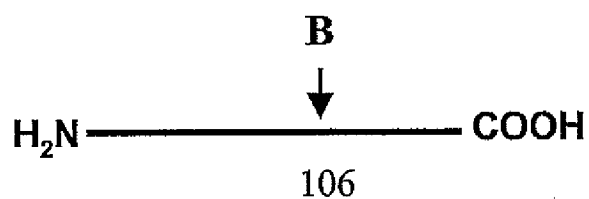
Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;
a-h, j-m, r-z = 0;
n = 1; R' = -Gal-linker-transferrin.

FIG. 28N

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a-c, e, f (independently selected) = 0 or 1;
 d, g = 0; R = polymer, glycoconjugate.

FIG. 280

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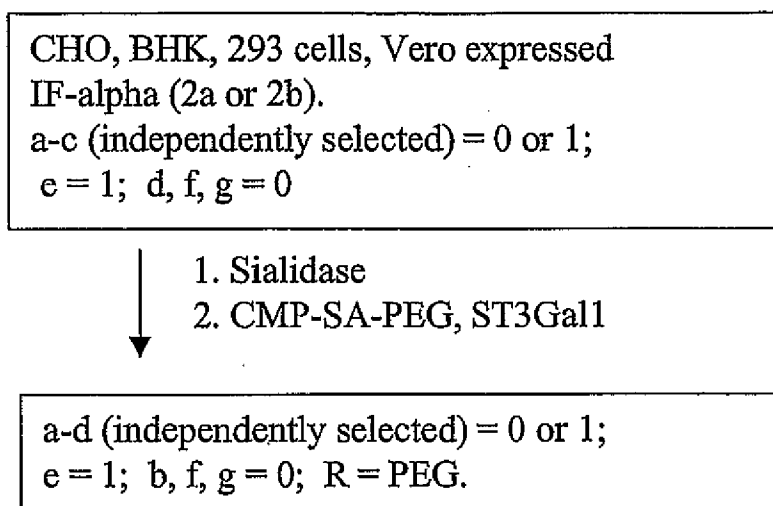


FIG. 28P

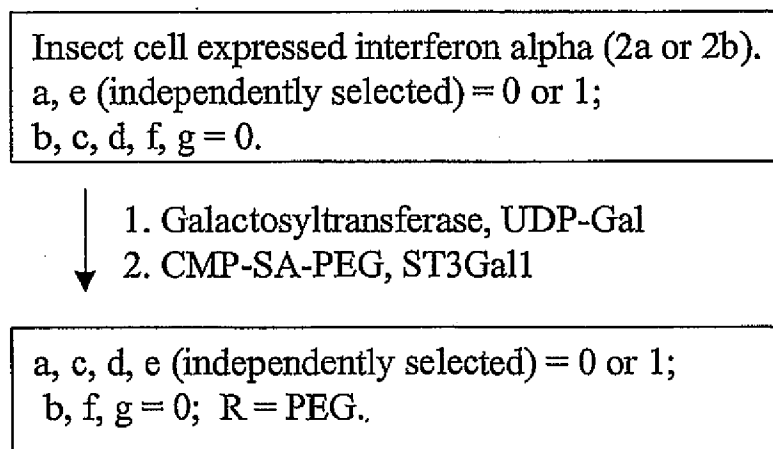


FIG. 28Q

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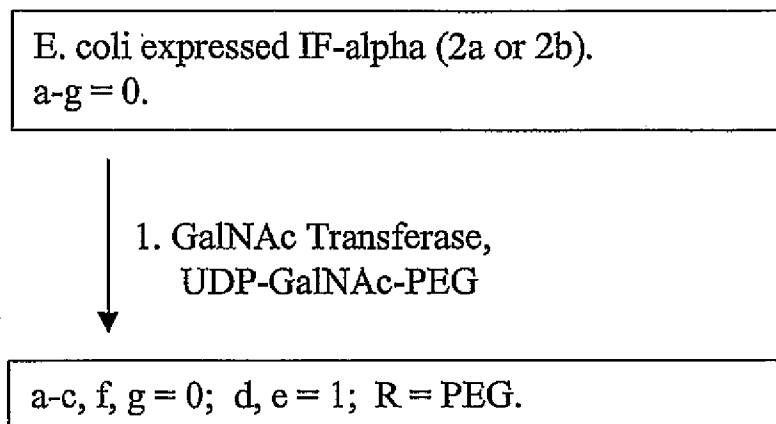


FIG. 28R

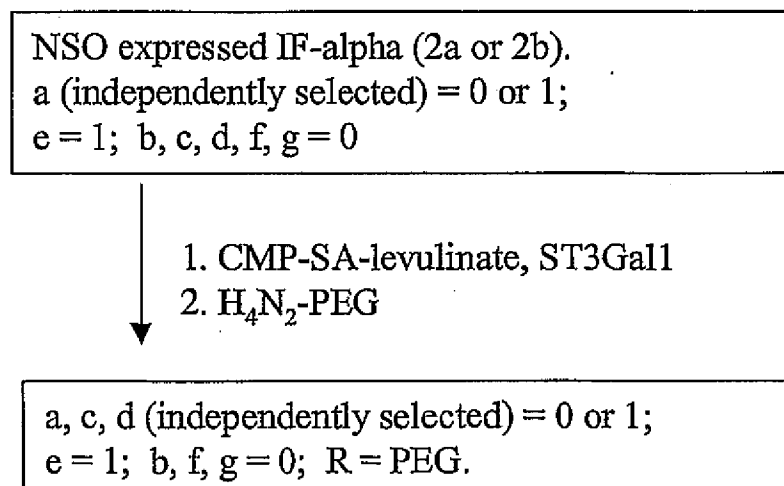


FIG. 28S

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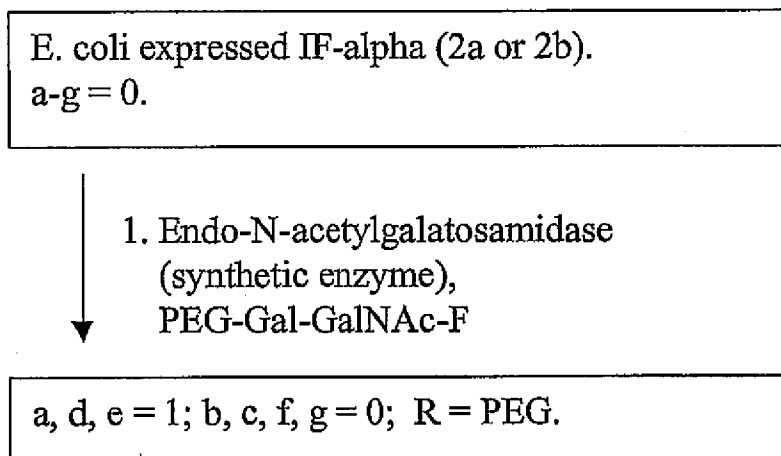


FIG. 28T

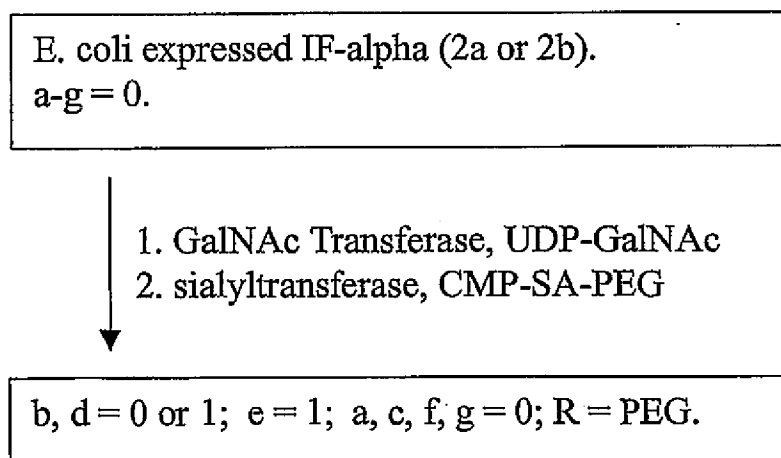


FIG. 28U

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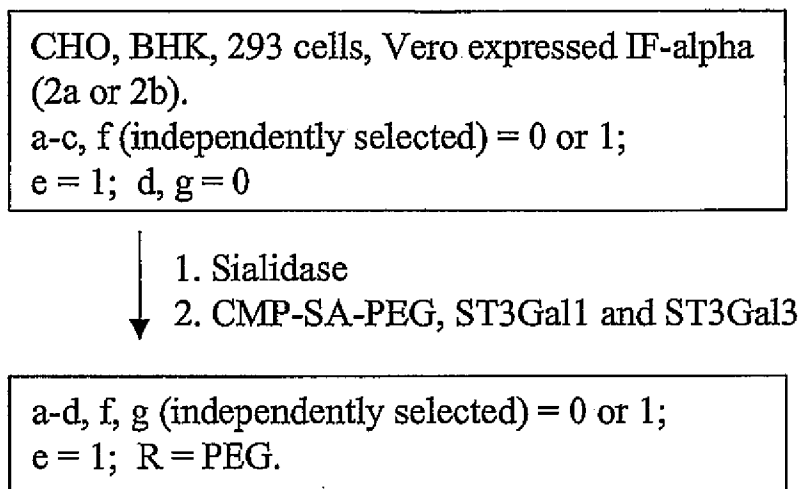


FIG. 28V

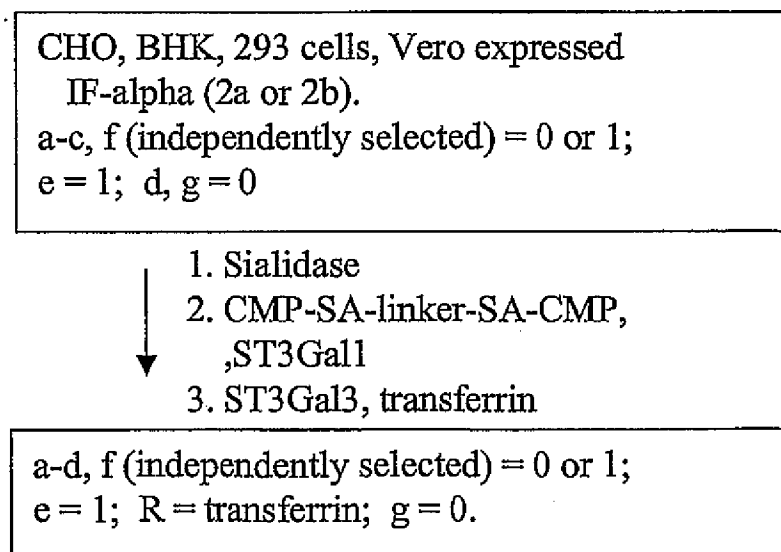
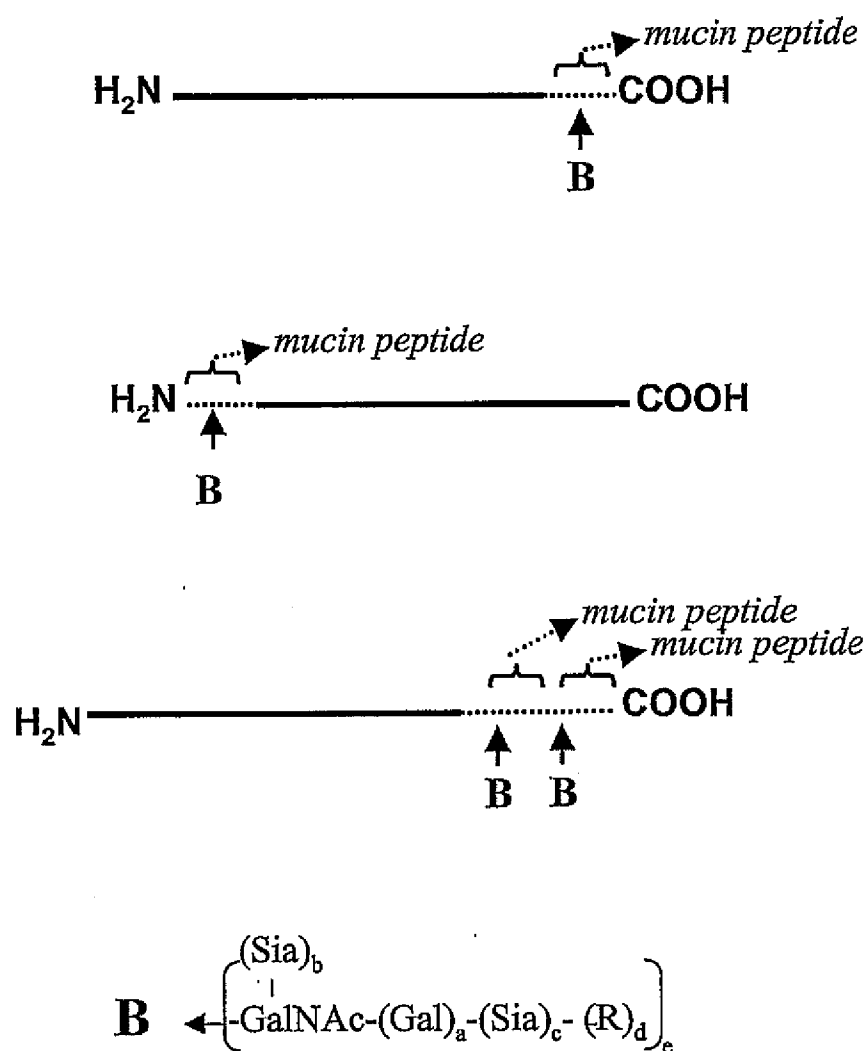


FIG. 28W

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer, glycoconjugate.

FIG. 28X

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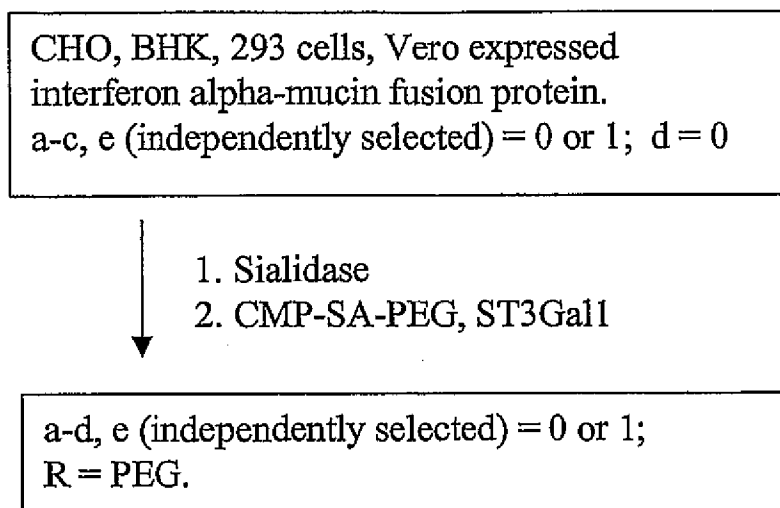


FIG. 28Y

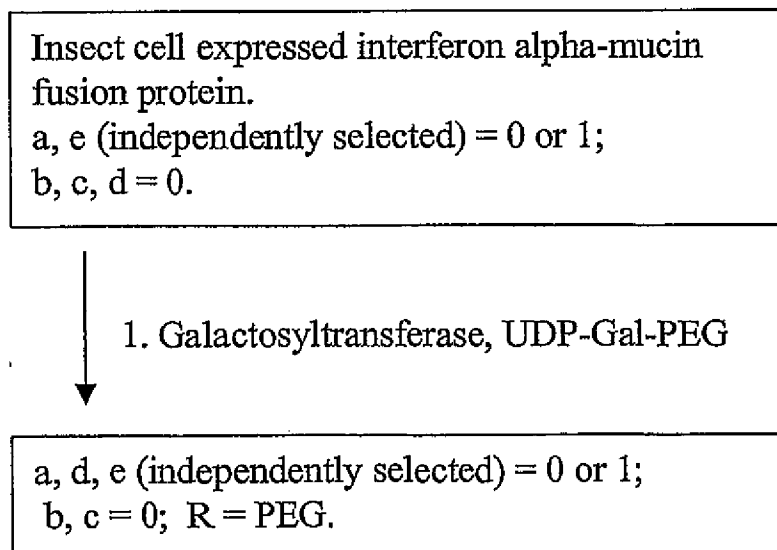


FIG. 28Z

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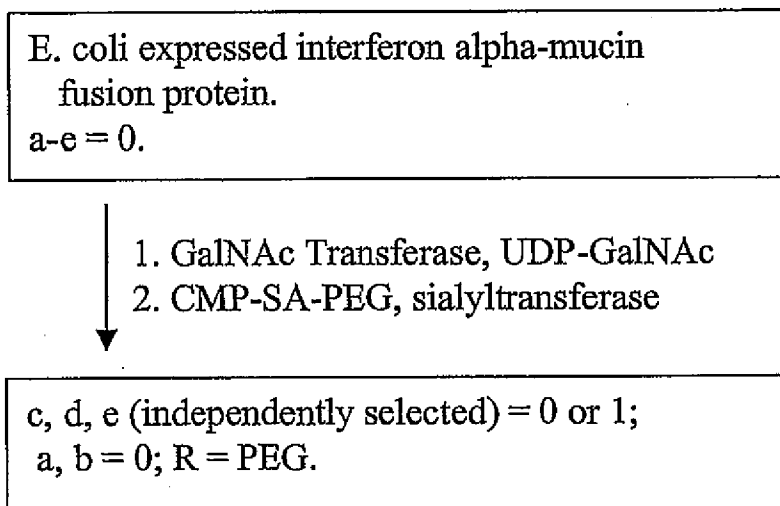
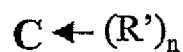
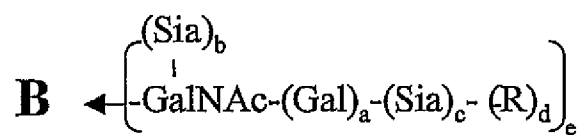
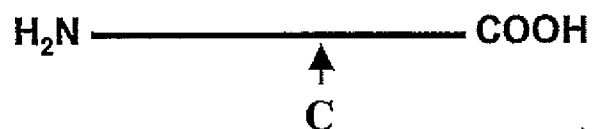
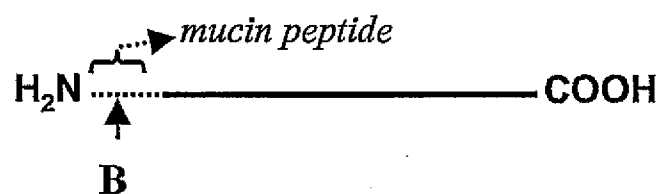
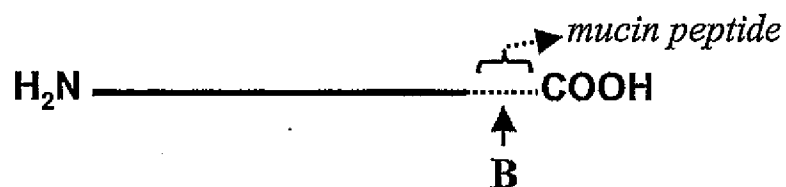


FIG. 28AA

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 28BB

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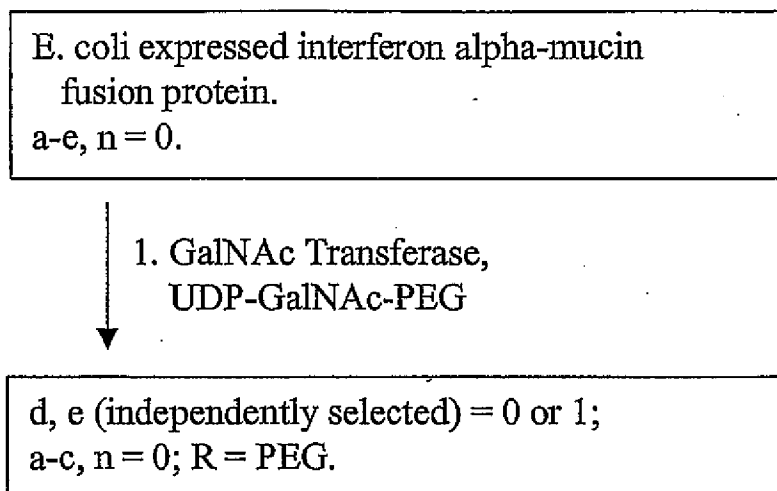


FIG. 28CC

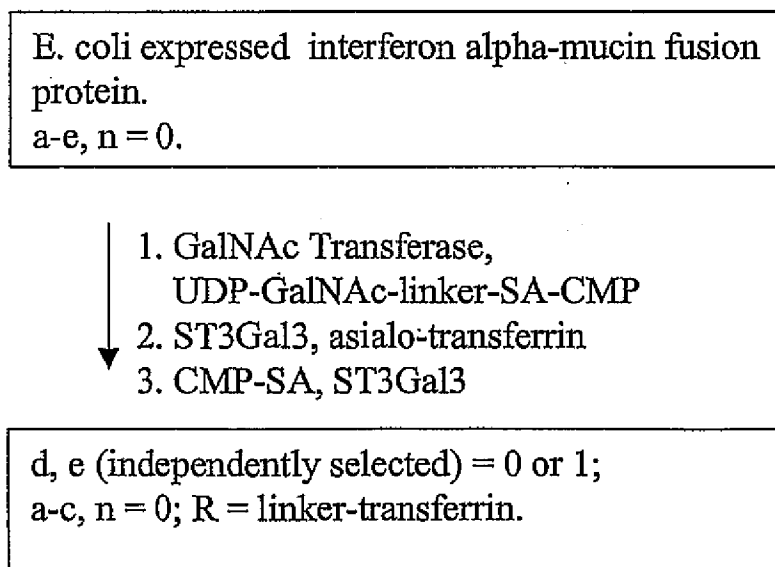


FIG. 28DD

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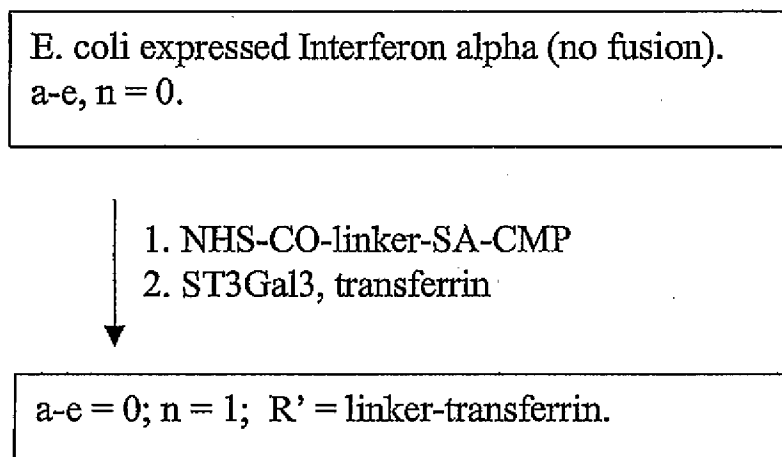
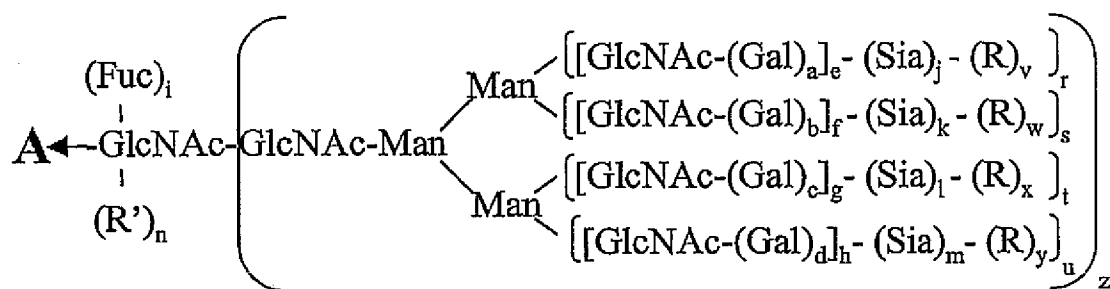
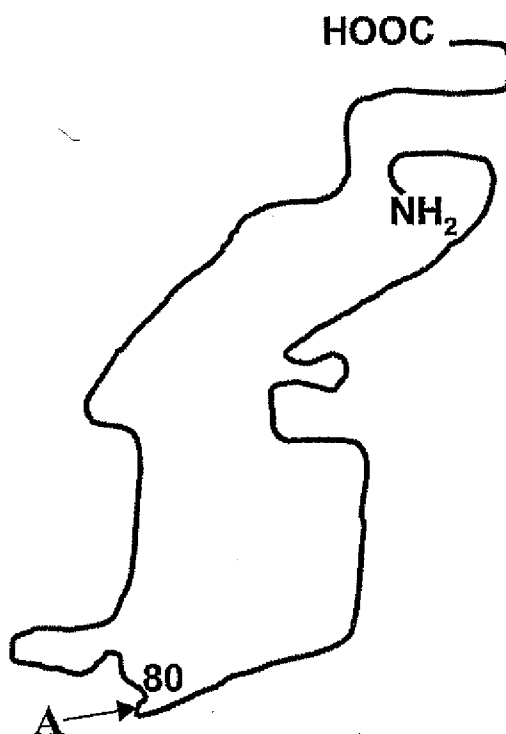


FIG. 28EE

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 29A

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CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 29B

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0 or 1;
 z = 1.



1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal3,
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 z = 1; R = PEG.

FIG. 29C

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Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 29D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 29E

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Insect cell expressed IF-beta

a-d, f, h, j-n, s, u, v-y = 0; e, g, i, r, t
(independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
z = 1; n = 0; R = PEG.

FIG. 29F

Yeast expressed IF-beta

a-n = 0; z = 1;
r-y (independently selected) = 0 to 1;
R (branched or linear) = Man, oligomannose.

- ↓
1. mannosidases
 2. GNT's 1,2,4,5, UDP-GlcNAc
 3. Galactosyltransferase, UDP-Gal
 - 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
z = 1; n = 0; R = PEG.

FIG. 29G

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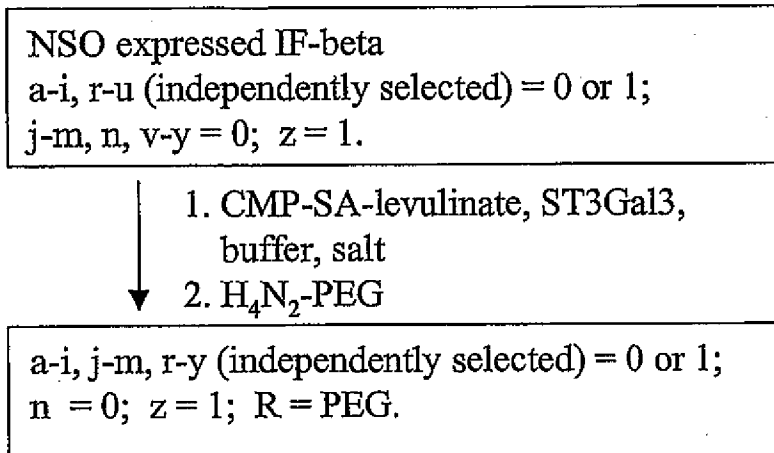


FIG. 29H

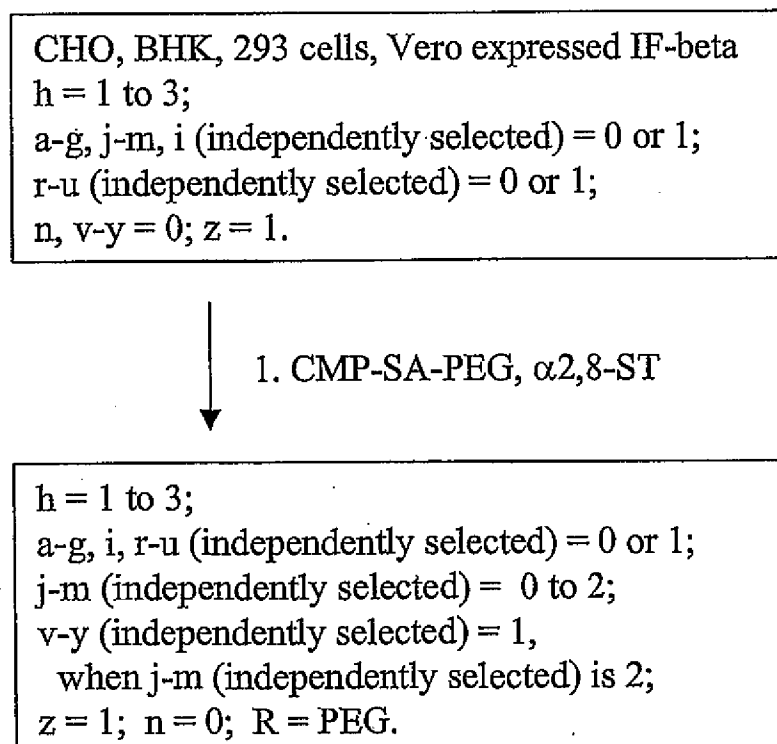


FIG. 29I

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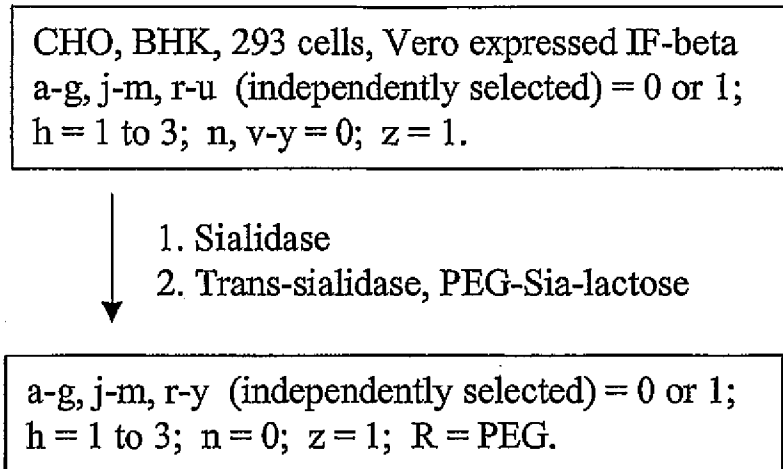


FIG. 29J

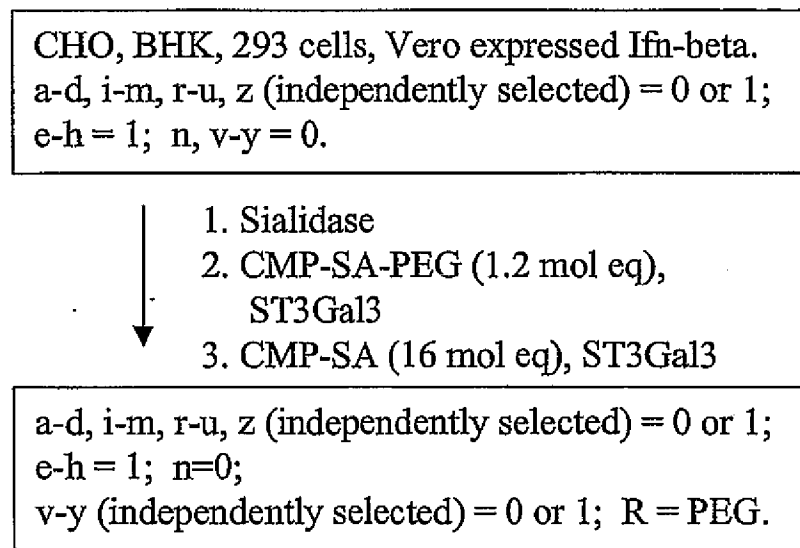


FIG. 29K

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NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

FIG. 29L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 29M

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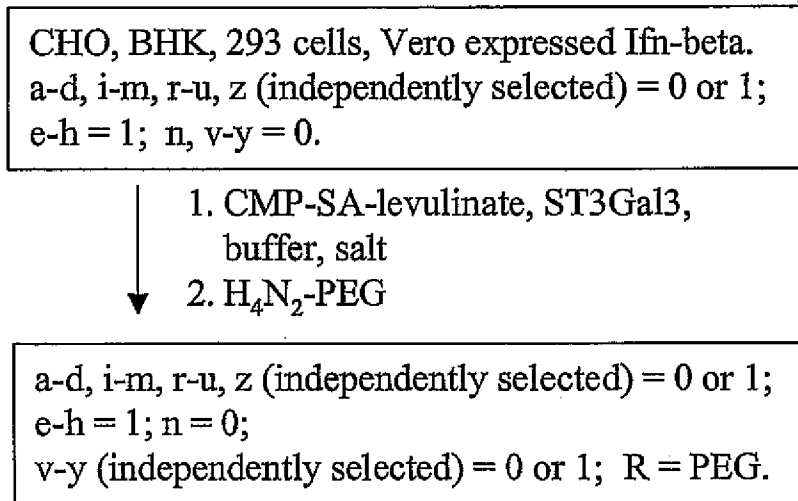


FIG. 29N

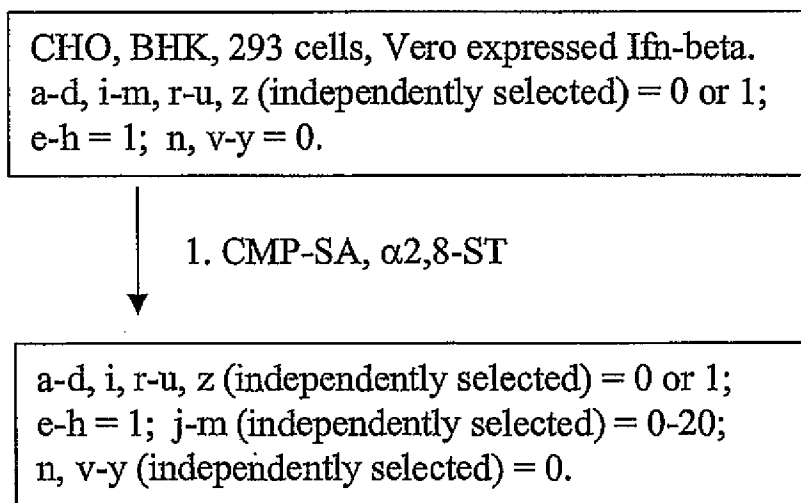
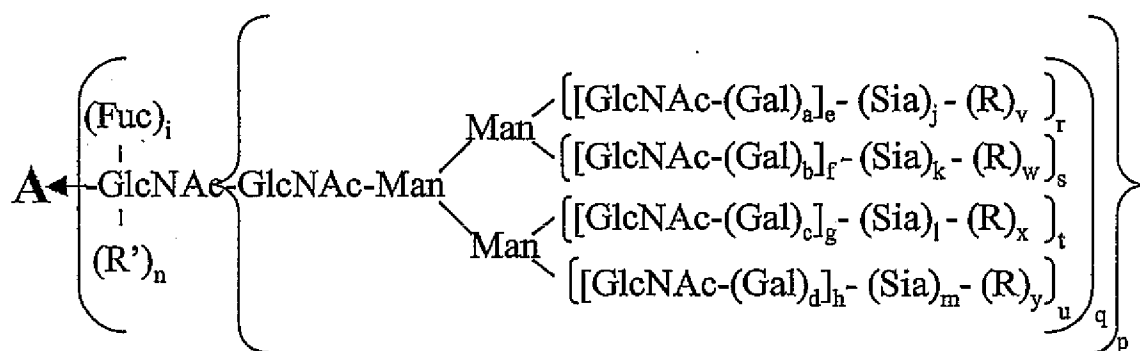
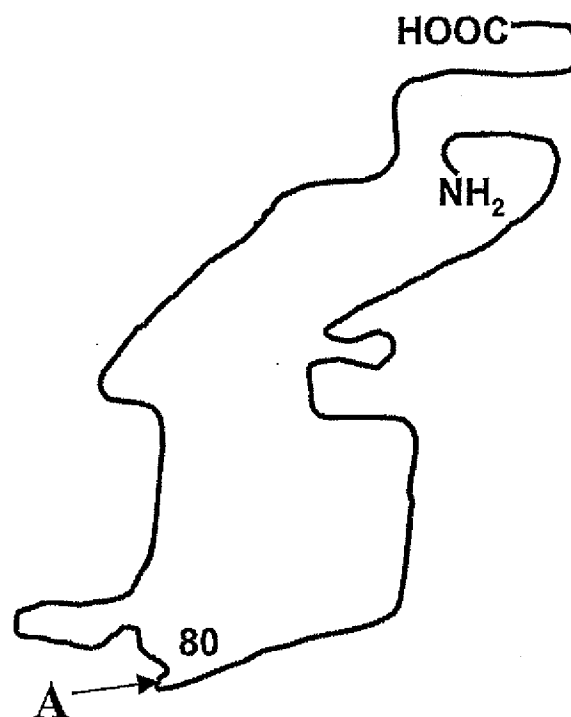


FIG. 29O

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,
glycoconjugate.

FIG. 29P

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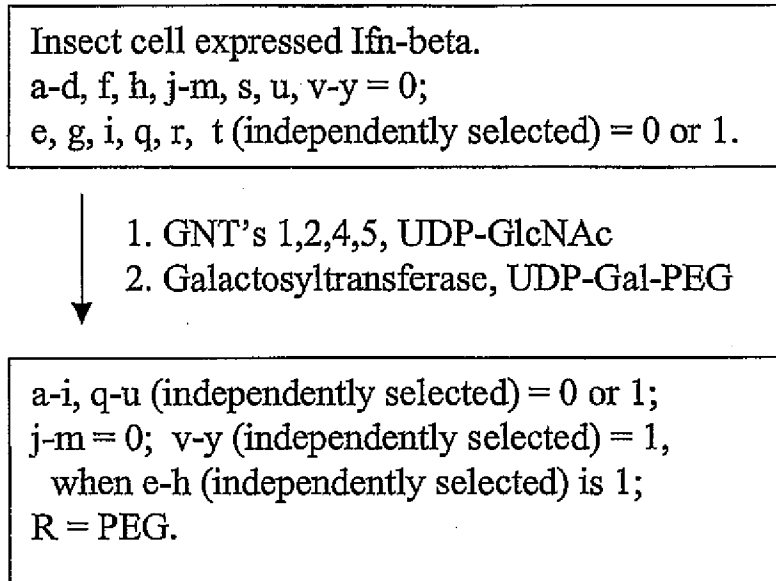


FIG. 29Q

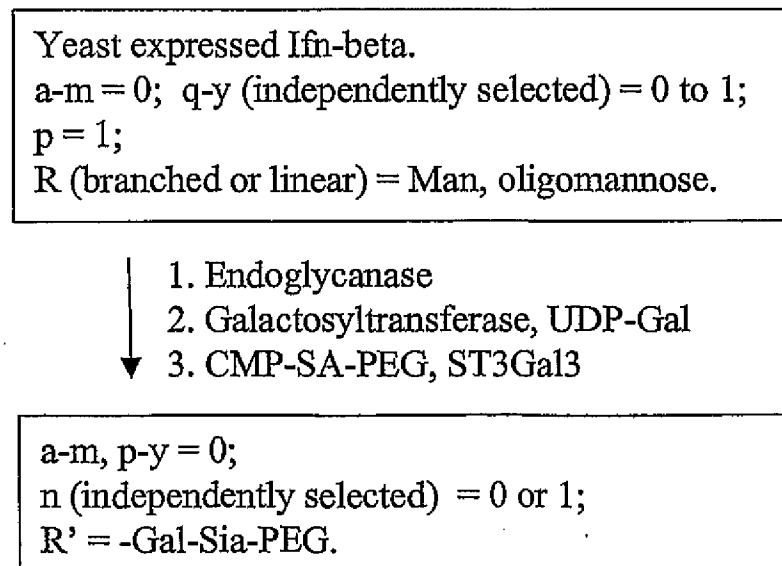


FIG. 29R

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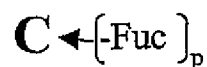
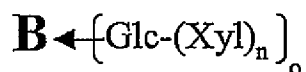
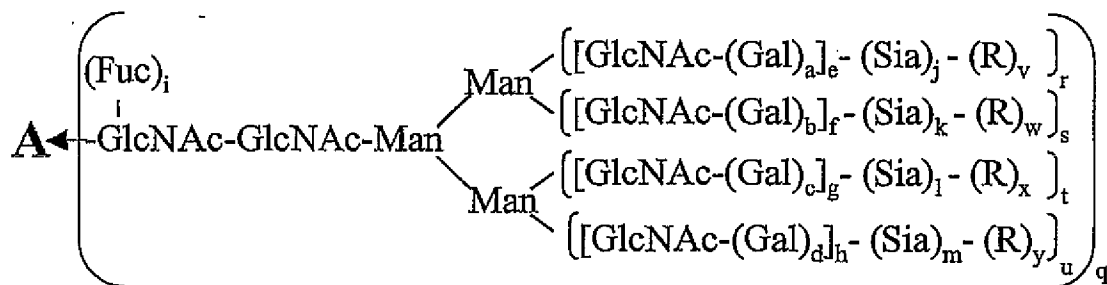
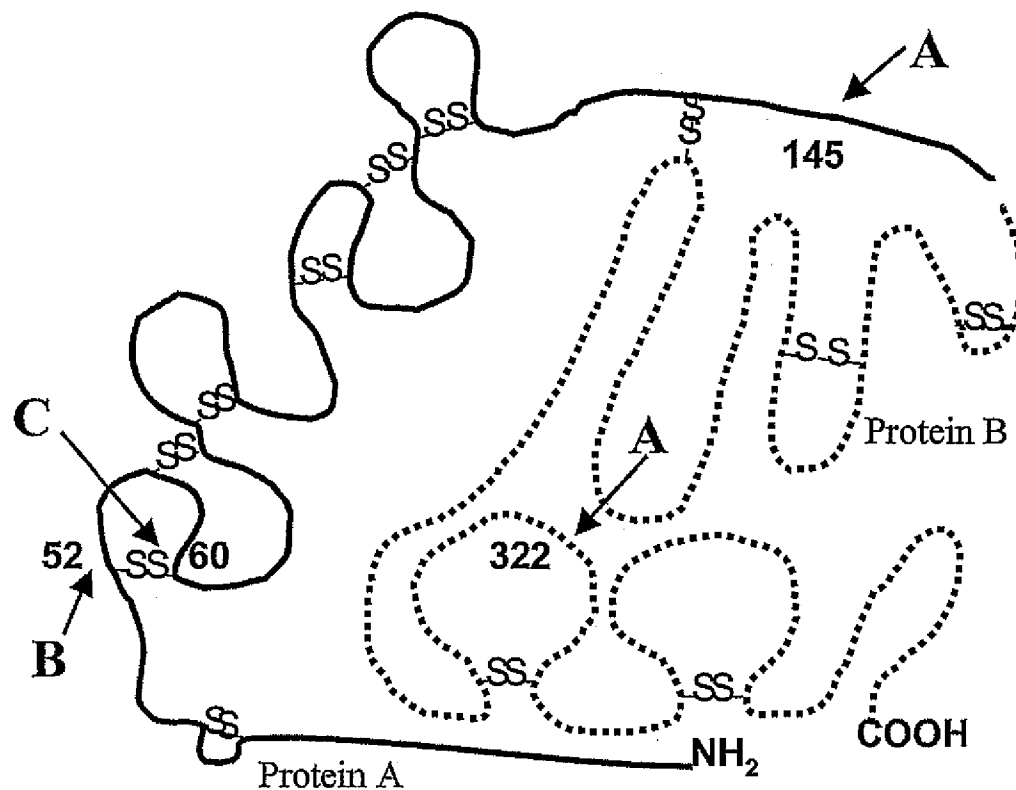
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

1. CMP-SA-linker-SA-CMP,
ST3Gal3
↓
2. ST3Gal3, desialylated transferrin.
3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 29S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 30A

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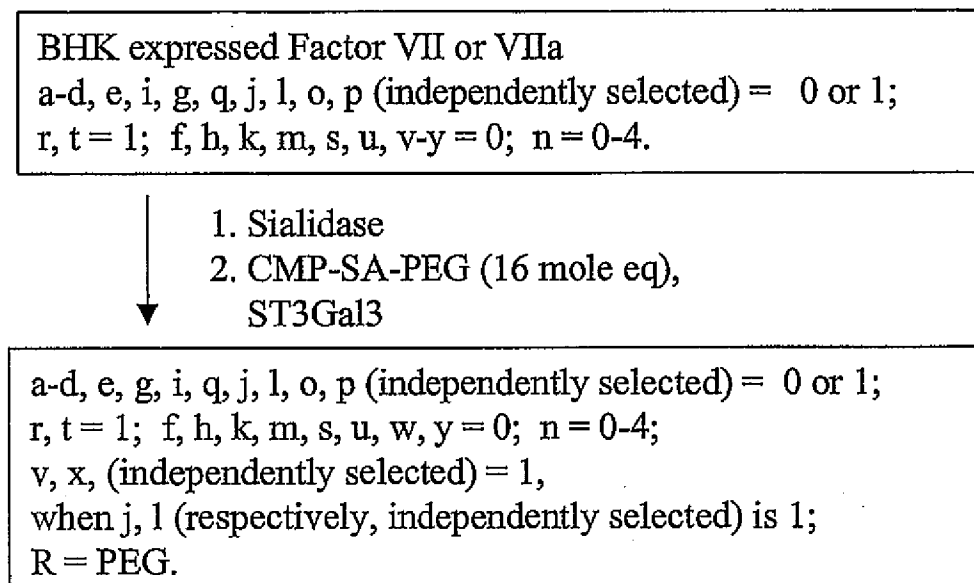


FIG. 30B

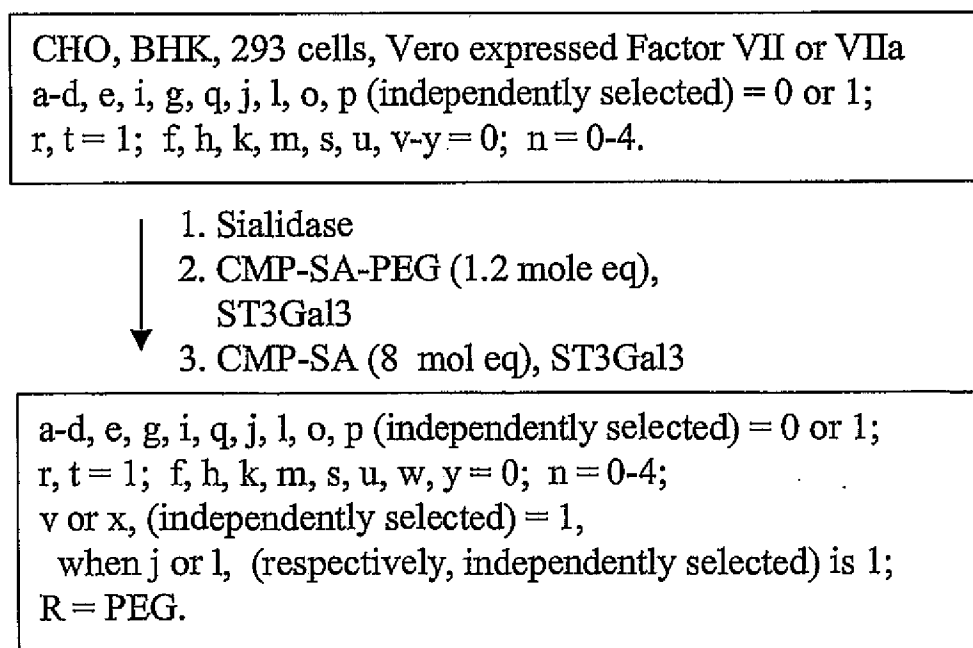


FIG. 30C

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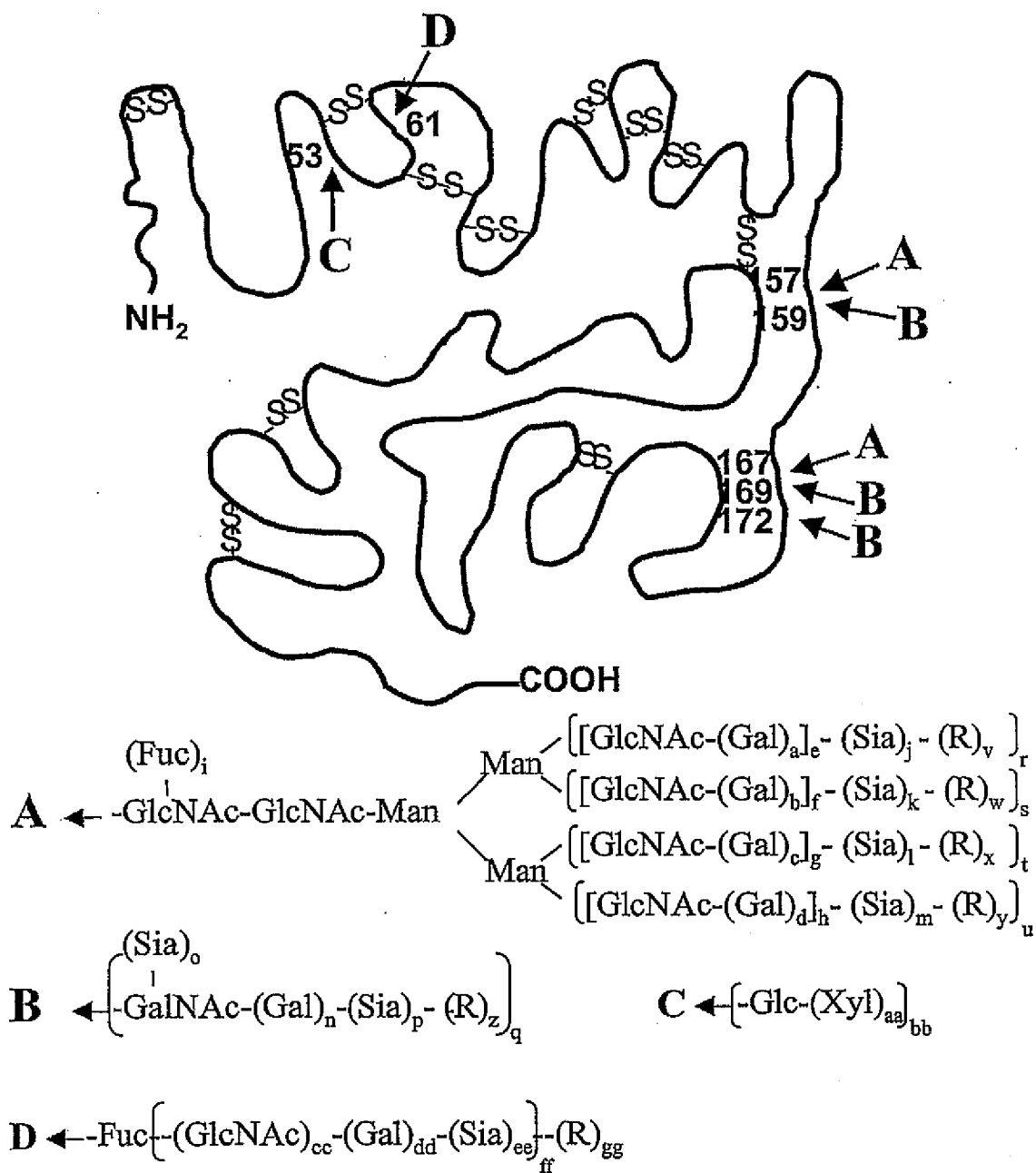
NSO expressed Factor VII or VIIa
a--u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 30D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 31A

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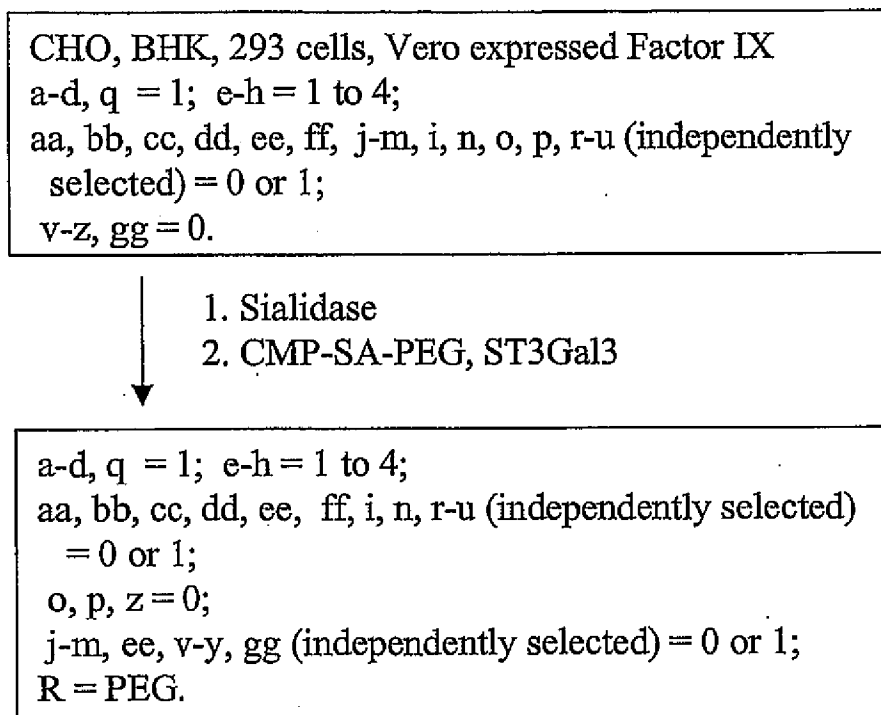


FIG. 31B

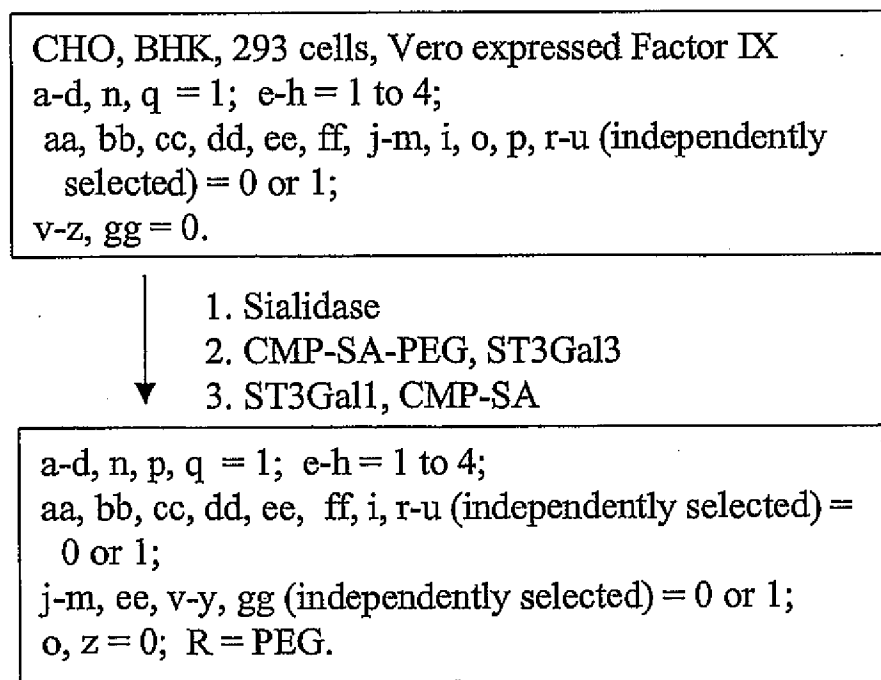


FIG. 31C

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1; R = PEG;
 o, v-y, gg = 0;
 j-m, p, ee (independently selected) = 0 or 1, but when
 p = 1, z = 1.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
- CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1; R = PEG;
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =
 0 or 1.

FIG. 31E

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 31F

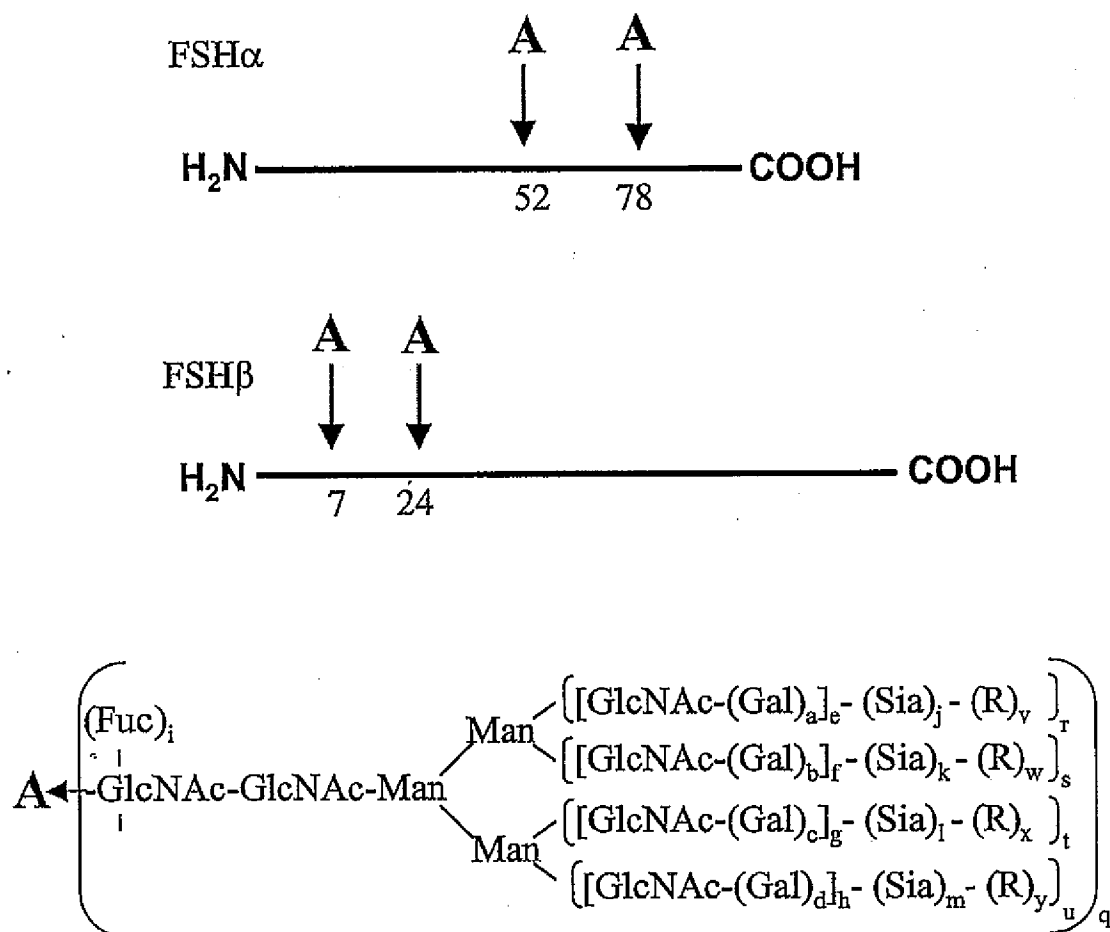
CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1;
 e-h, aa = 1 to 4;
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α2,8-ST

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee (independently selected) = 0 to 2;
 v-y, gg (independently selected) = 1, when j-m
 (independently selected) is 2;

FIG. 31G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 32A

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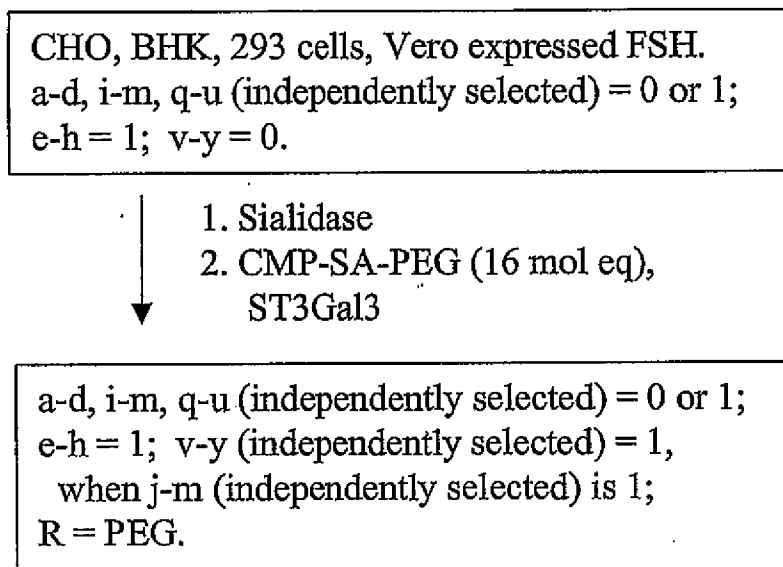


FIG. 32B

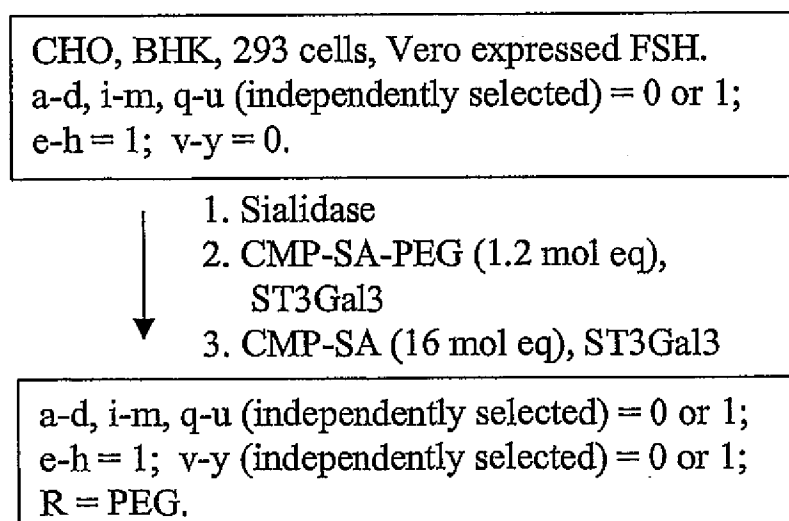


FIG. 32C

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NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-PEG, ST3Gal1

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 32D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ↓ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 32E

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CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 32F

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 32G

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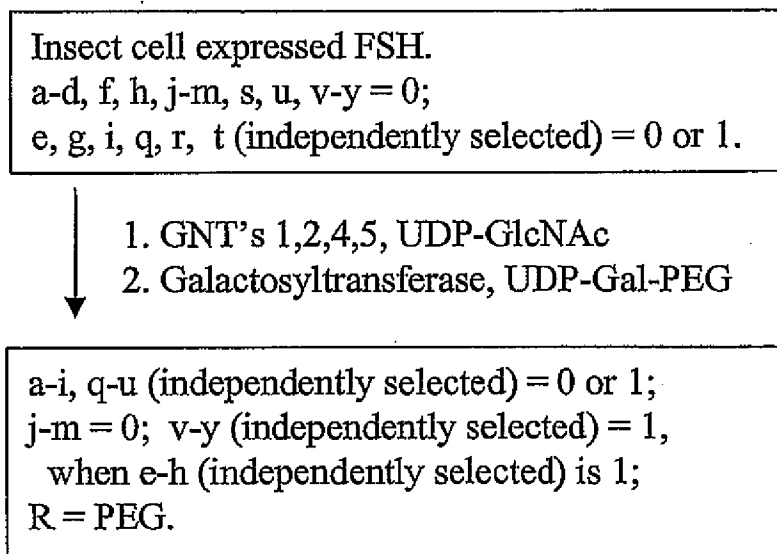


FIG. 32H

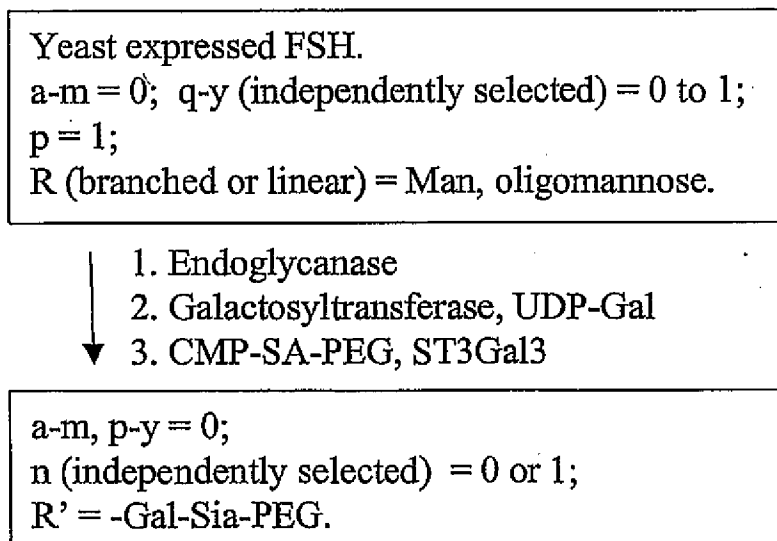


FIG. 32I

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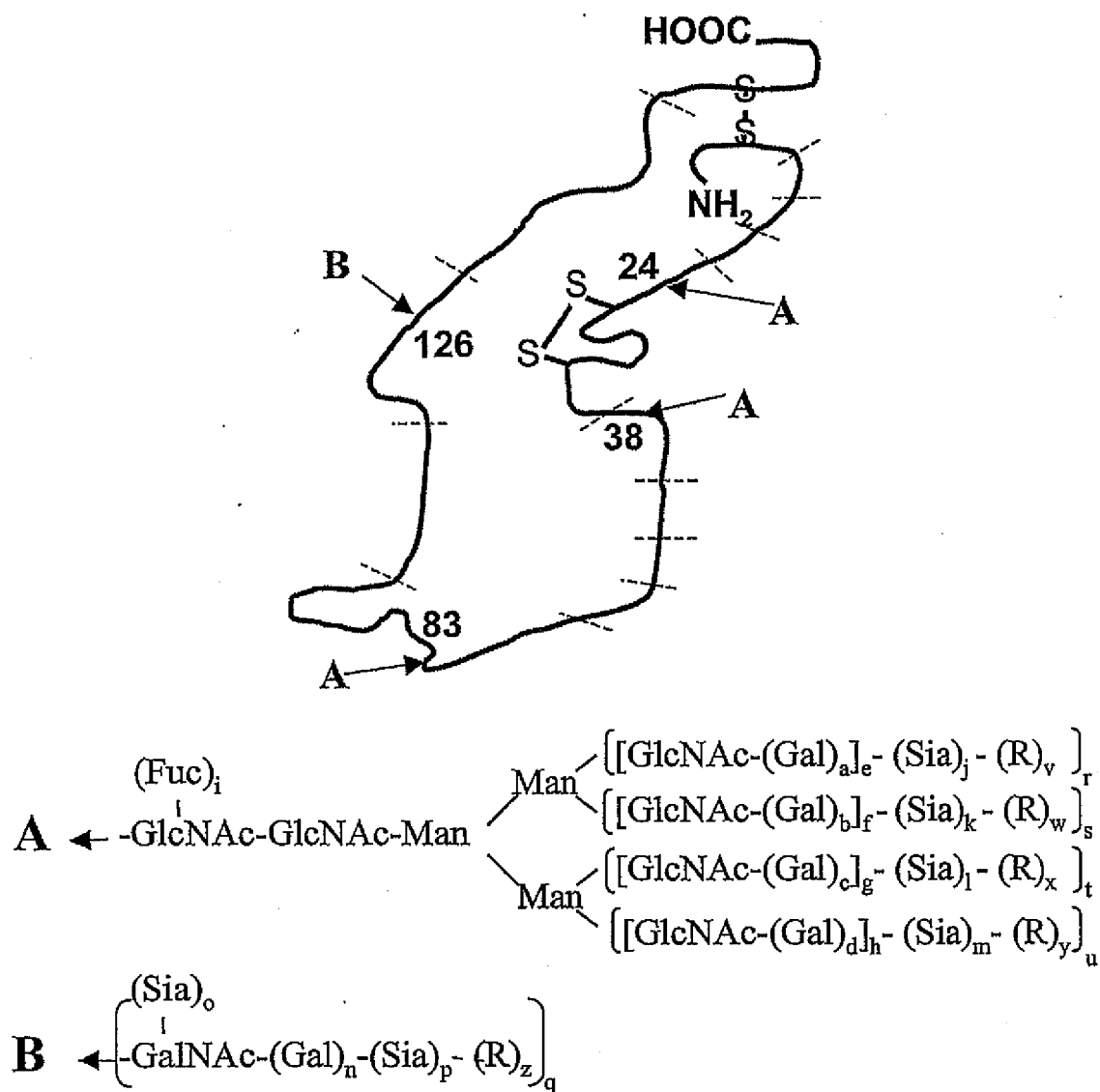
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 32J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 33A

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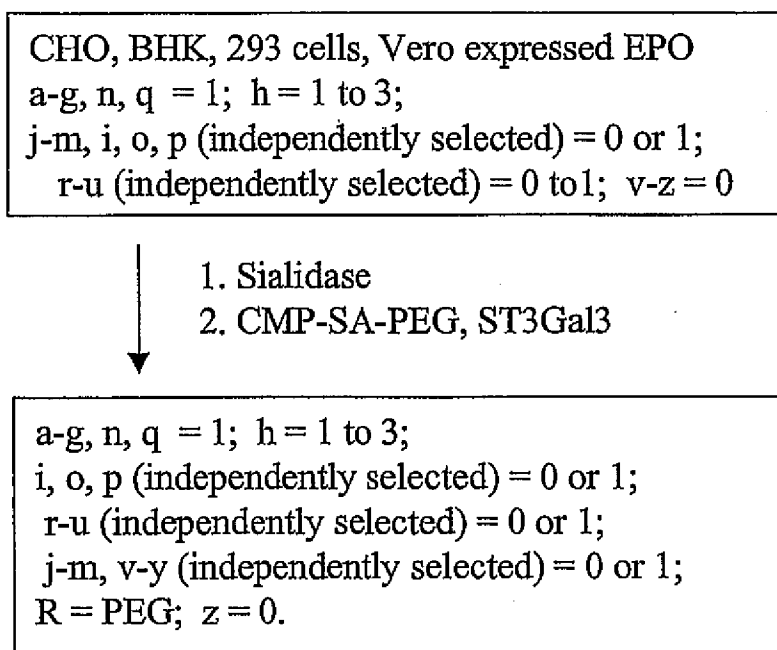


FIG. 33B

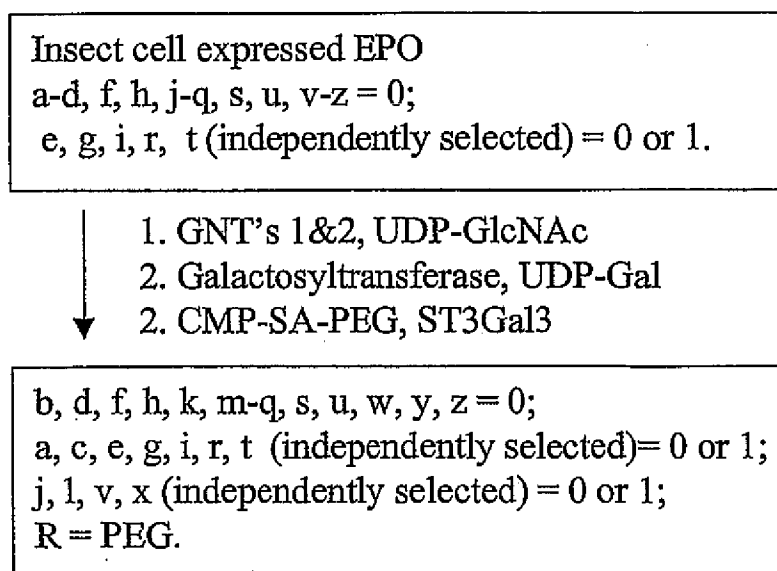


FIG. 33C

110/345

CHO, BHK, 293 cells, Vero expressed EPO
 a-q, r-u (independently selected) = 0 or 1;
 v-z = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 - ↓ 4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;
 i-m, o, r-u (independently selected) = 0 or 1;
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 v-z = 0

- ↓
1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 33E

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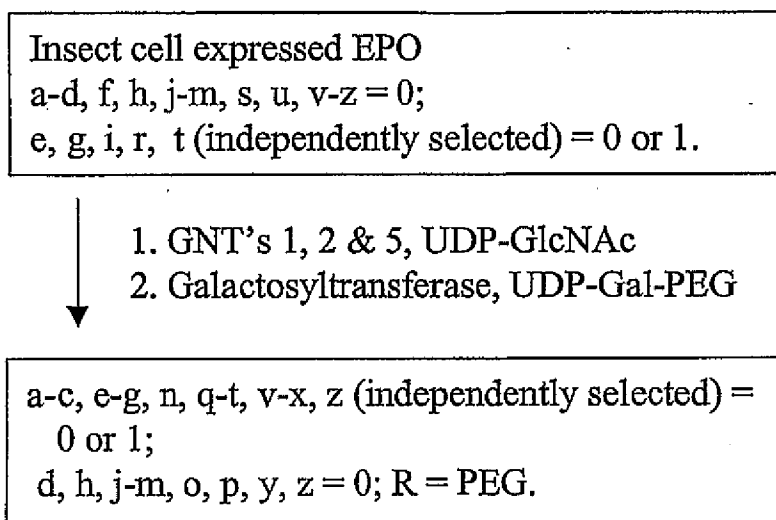


FIG. 33F

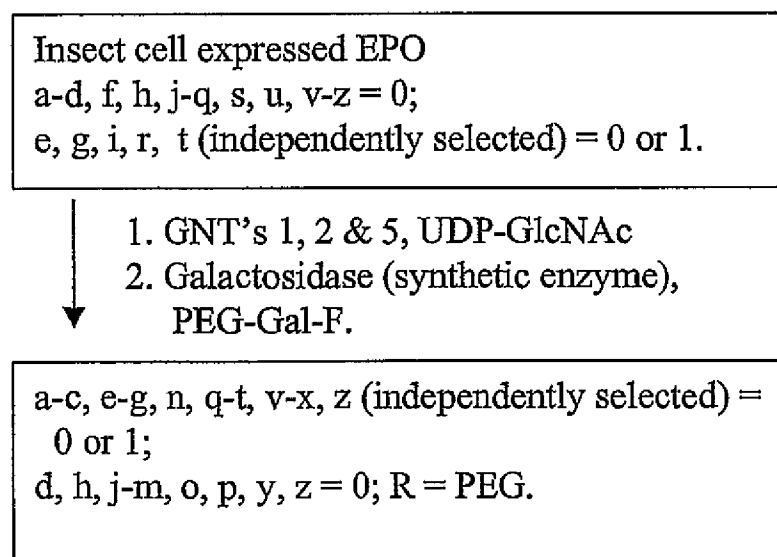


FIG. 33G

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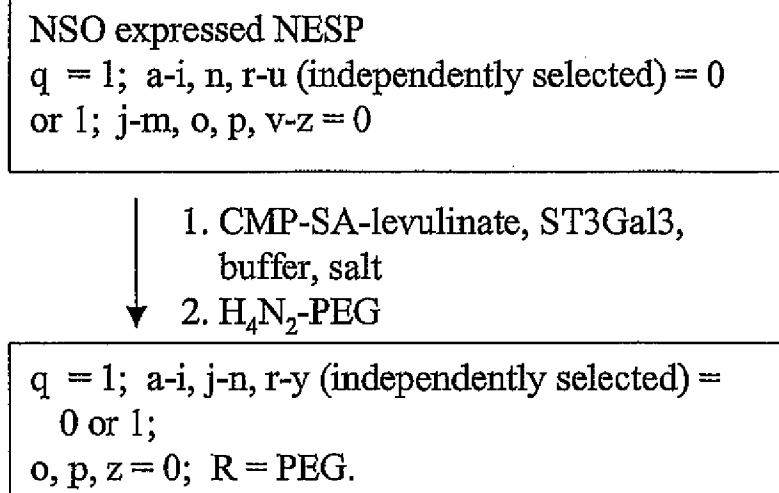


FIG. 33H

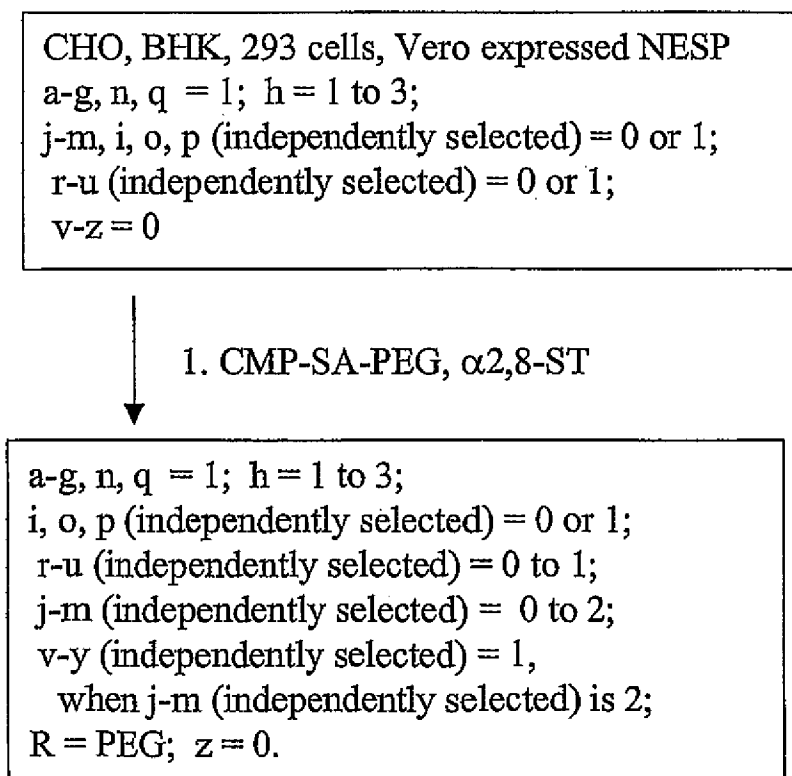


FIG. 33I

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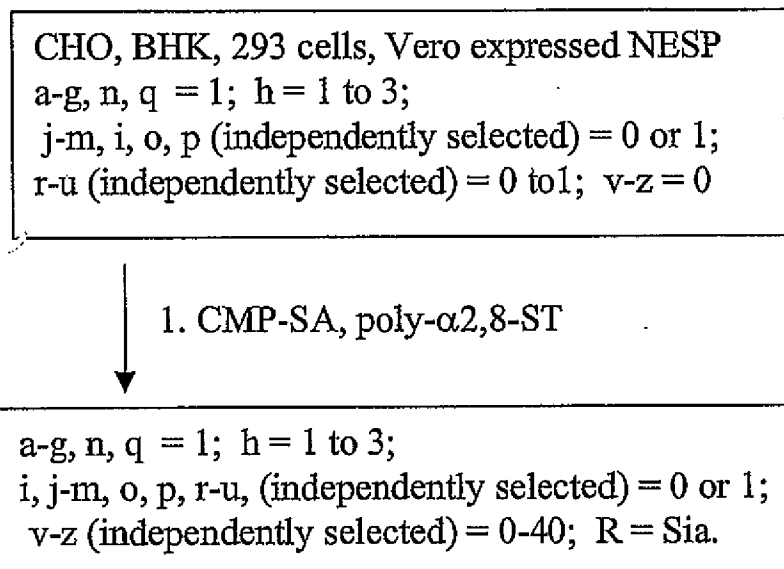
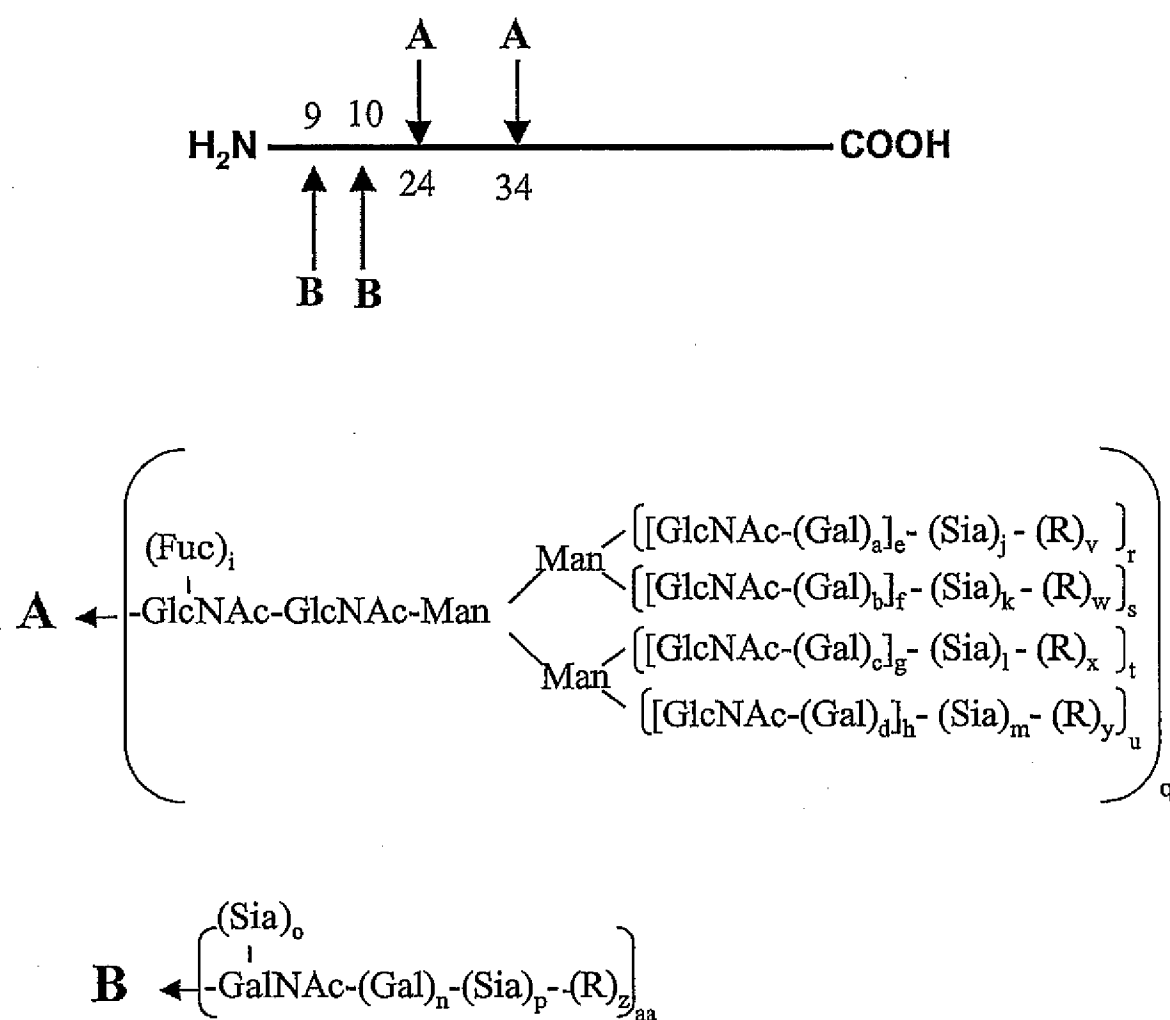


FIG. 33J

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a-d, i, n-u, aa (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer, glycoconjugate.

FIG. 34A

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
 o, p, z = 0; n, e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 34B

CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 - ↓ 3. CMP-SA (16 mol eq), ST3Gal3 &
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;
 o, z = 0; n, e-h = 1;
 v-y (independently selected) = 0 or 1; R = PEG.

FIG. 34C

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NSO expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-PEG, ST3Gal1

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;

n, e-h = 1; o, v-y = 0; z = 1, when p = 1; R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-y, aa (independently selected) = 0 or 1;

o, p, z = 0; n, e-h = 1; R = PEG.

FIG. 34E

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = PEG.

FIG. 34F

CHO, BHK, 293 cells, Vero expressed GMCSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; j-m (independently selected) = 0-20;
v-z (independently selected) = 0.

FIG. 34G

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Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

e, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 34I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. Endoglycanase
 2. mannosidase (if aa = 1).
 3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;

q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 34J

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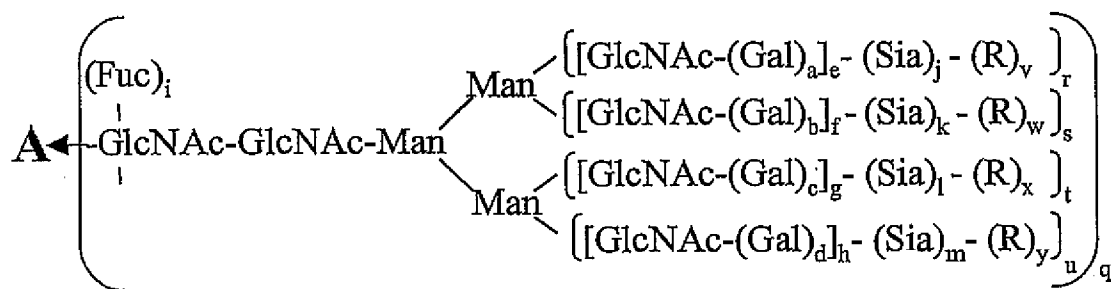
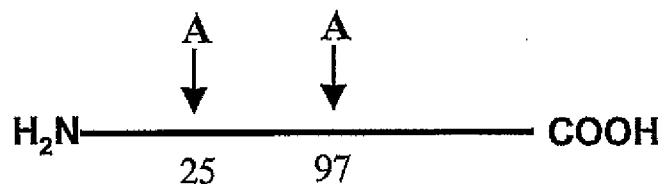
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 34K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 35A

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CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 35B

CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 35C

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NSO expressed Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed

Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 35E

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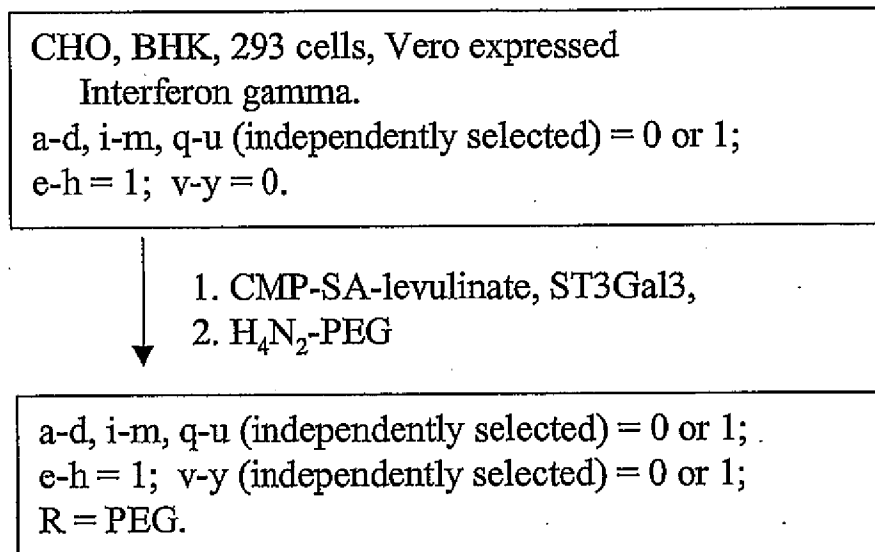


FIG. 35F

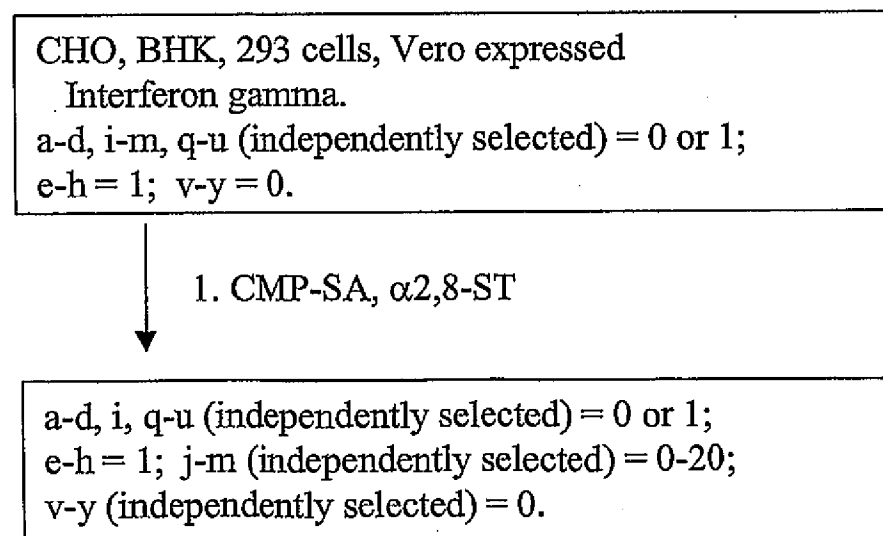
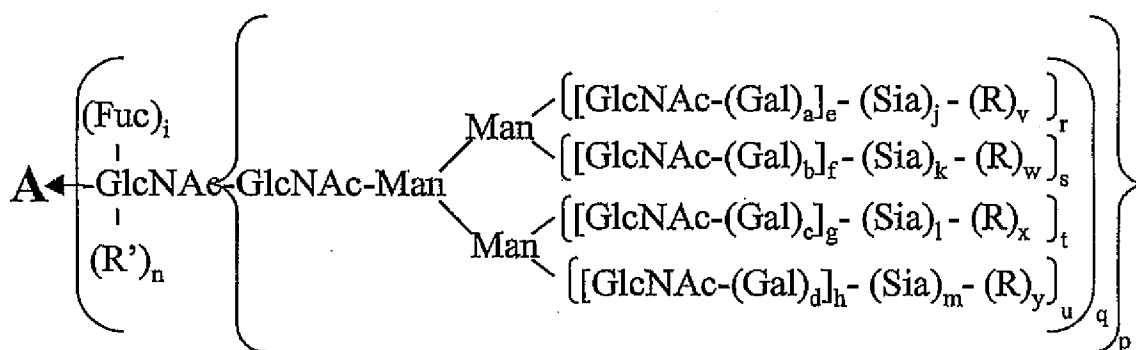
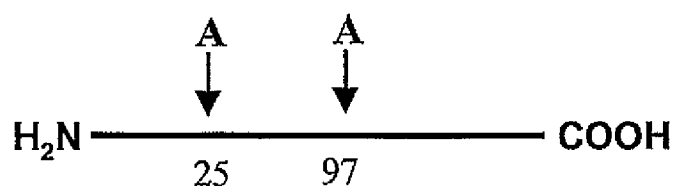


FIG. 35G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 35H

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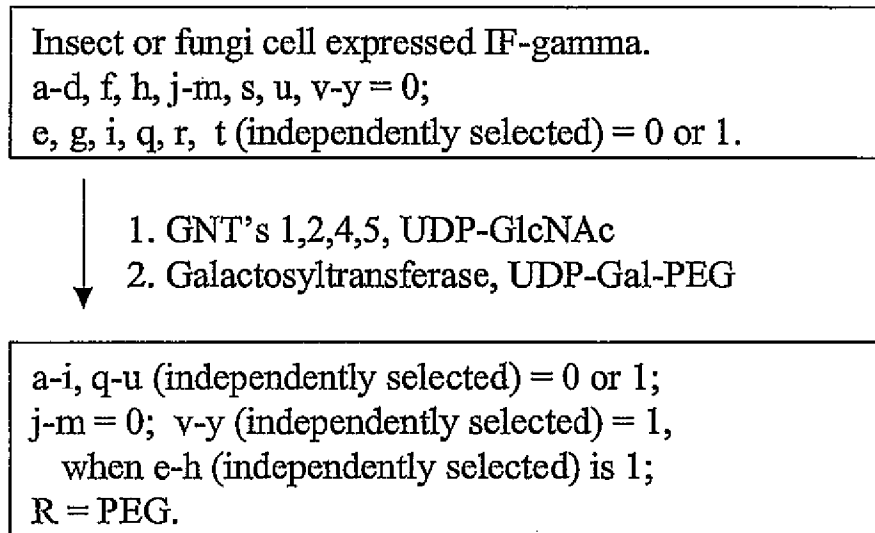


FIG. 35I

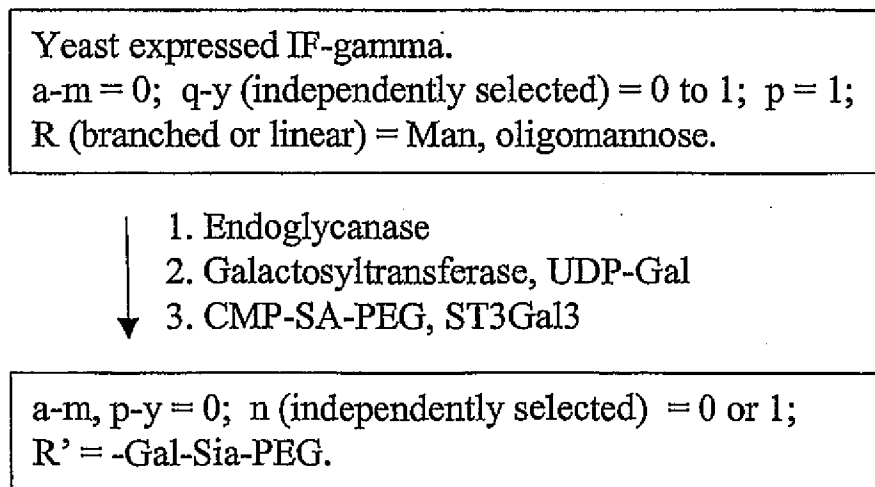


FIG. 35J

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CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
 2. Galactosyltransferase, transferrin treated with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 35K

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1;
n, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 35L

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Insect or fungi cell expressed IF-gamma.
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1 & 2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
 e, g, i, r, t, q (independently selected) = 0 or 1;
 p = 1; v, x (independently selected) = 1,
 when e, g (independently selected) is 1;
 R = PEG.

FIG. 35M

CHO, BHK, 293 cells, Vero expressed
 Interferon gamma.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

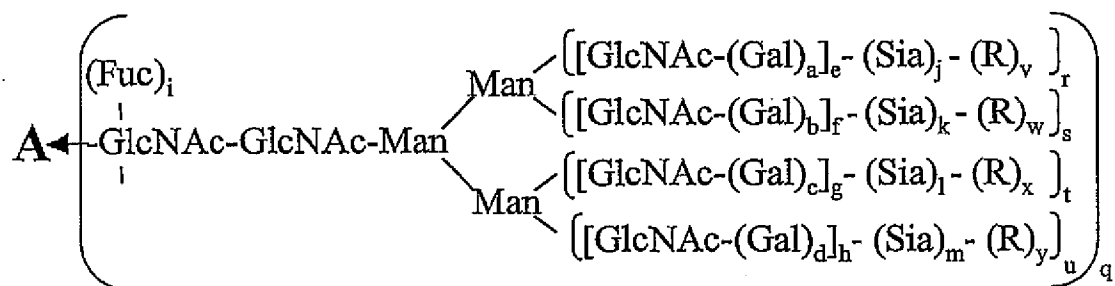
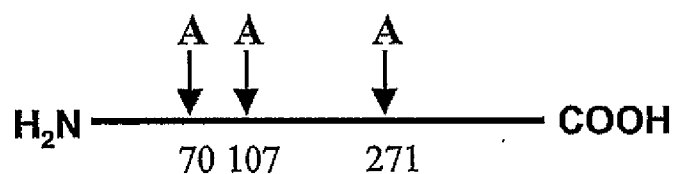


1. CMP-SA-PEG, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
 e-h = 1; j-m (independently selected) = 0-2;
 v-y (independently selected) = 1,
 when j-m (independently selected) = 2;
 R = PEG.

FIG. 35N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 36A

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed α_1 antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero or transgenic
animal expressed α_1 antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 36C

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NSO expressed α_1 -antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1;

v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 36D

CHO, BHK, 293 cells, Vero or transgenic animal
expressed alpha-1 antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 36E

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed α_1 -antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 36F

CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.

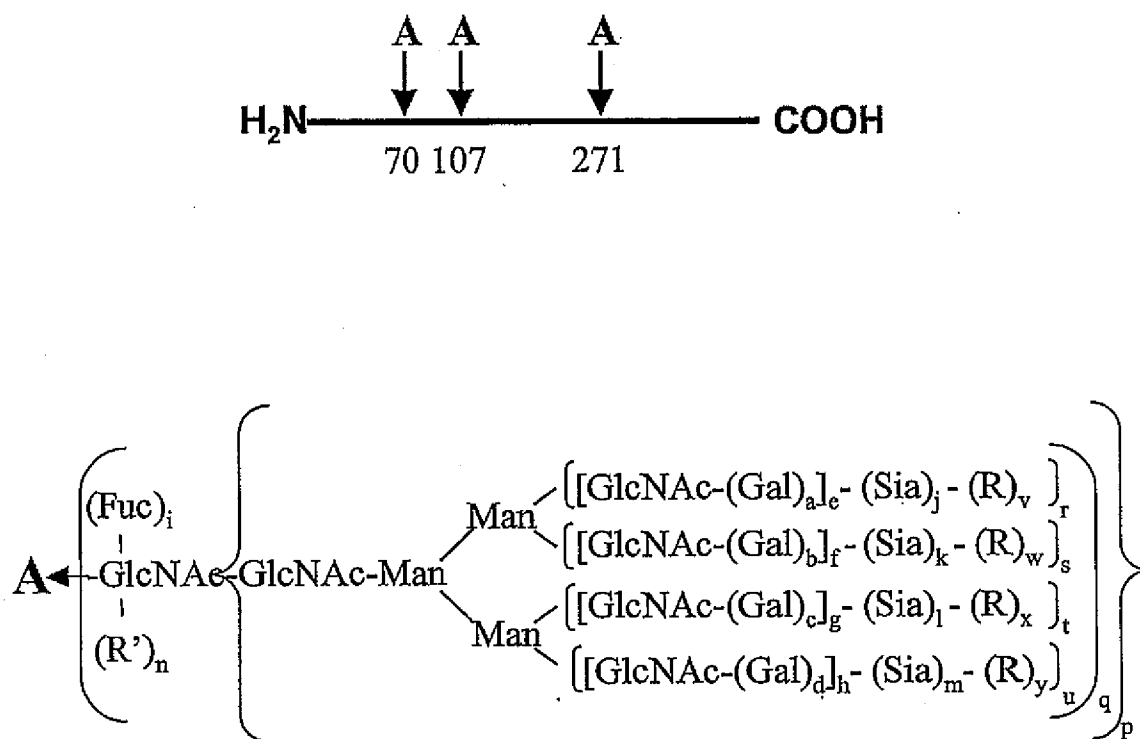
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, $\alpha_{2,8}$ -ST

a-d, i, q-u (independently selected) = 0 or 1; e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 36G

133/345



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

134/345

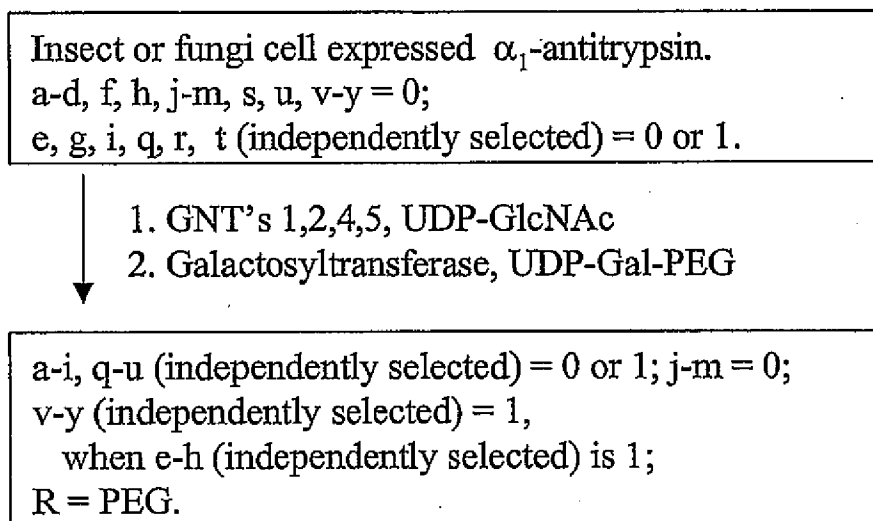


FIG. 36I

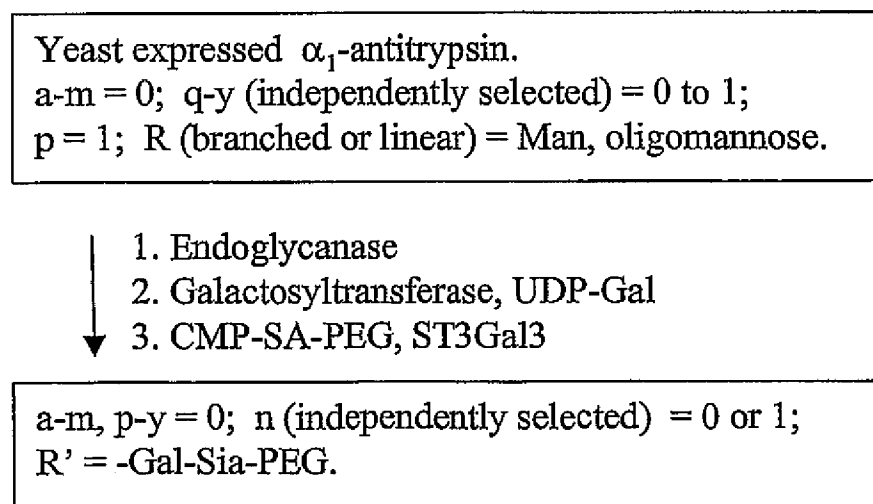


FIG. 36J

135/345

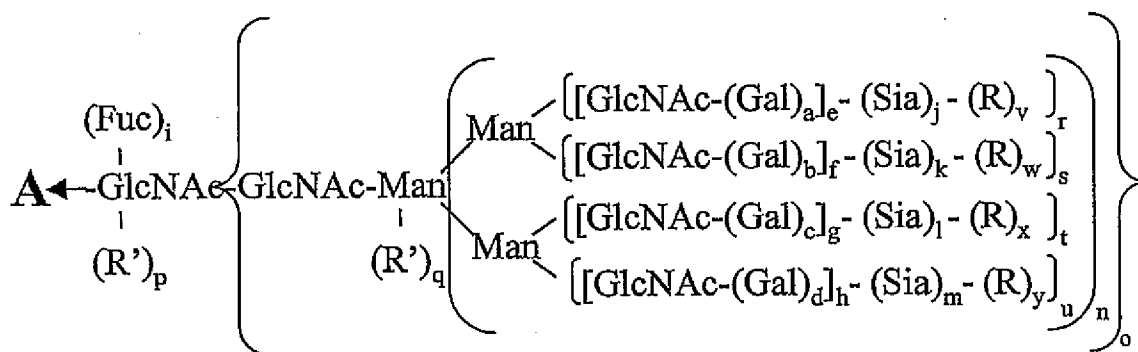
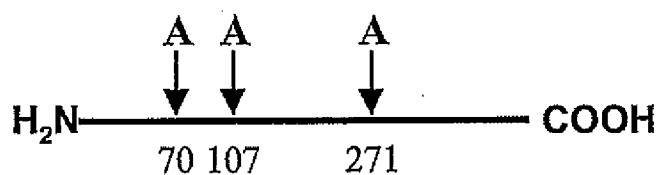
CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin treated
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 36K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 36L

137/345

Yeast expressed alpha-1 antitrypsin.
 a-h, i-m, p, q = 0;
 R (independently selected) = mannose, oligomannose,
 polymannose;
 r-u, v-y (independently selected) = 0 or 1; n, o = 1.

- ↓ 1. endoglycanase
 ↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.
 R'' = Gal-PEG.

FIG. 36M

Plant expressed alpha-1 antitrypsin.
 a-d, f, h, j-m, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1;
 n=1; R' = xylose

- ↓ 1. hexosaminidase,
 ↓ 2. alpha mannosidase and xylosidase
 ↓ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0;
 q = 1; R' = GlcNAc-PEG.

FIG. 36N

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CHO, BHK, 293 cells, Vero, transgenic animal
expressed α_1 antitrypsin.
a-h, i-o, r-u (independently selected) = 0 or 1;
p, q, v-y = 0.

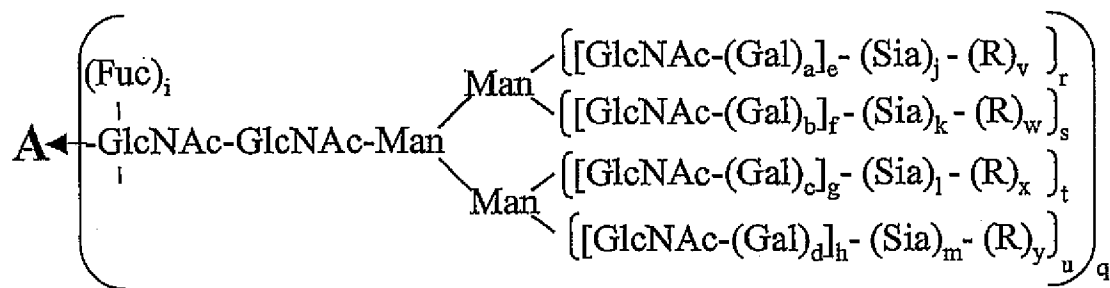
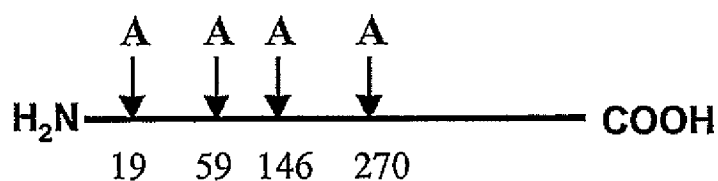


1. CMP-SA-PEG,
ST3Gal3

a-h, i-o, r-u (independently selected) = 0 or 1;
p, q = 0; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 360

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

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CHO, BHK, 293 cells, Vero expressed Cerezyme
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 37B

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-M-6-P (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = mannose-6-phosphate

FIG. 37C

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NSO expressed Cerezyme.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

↓ 1. Sialidase and α -galactosidase

2. α -Galactosyltransferase, UDP-Gal

↓ 3. CMP-SA-M-6-P, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = mannose-6 phosphate

FIG. 37D

CHO, BHK, 293 cells, Vero expressed Cerezyme.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

↓ 1. Sialidase

2. CMP-SA-PEG (16 mol eq),
ST3Gal3

↓ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = Mannose-6-phosphate

FIG. 37E

142/345

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt.
 2. H_4N_2 -spacer-M-6-P or clustered M-6-P

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = M-6-P or clustered M-6-P

FIG. 37F

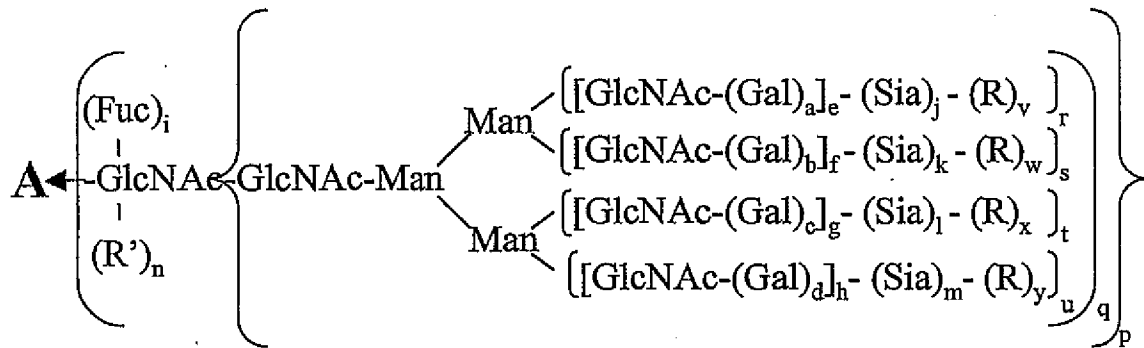
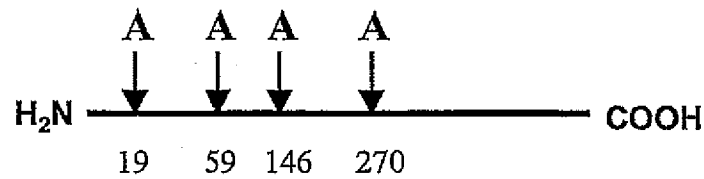
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, $\alpha 2,8$ -ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 37G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 37H

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Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 37I

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 37J

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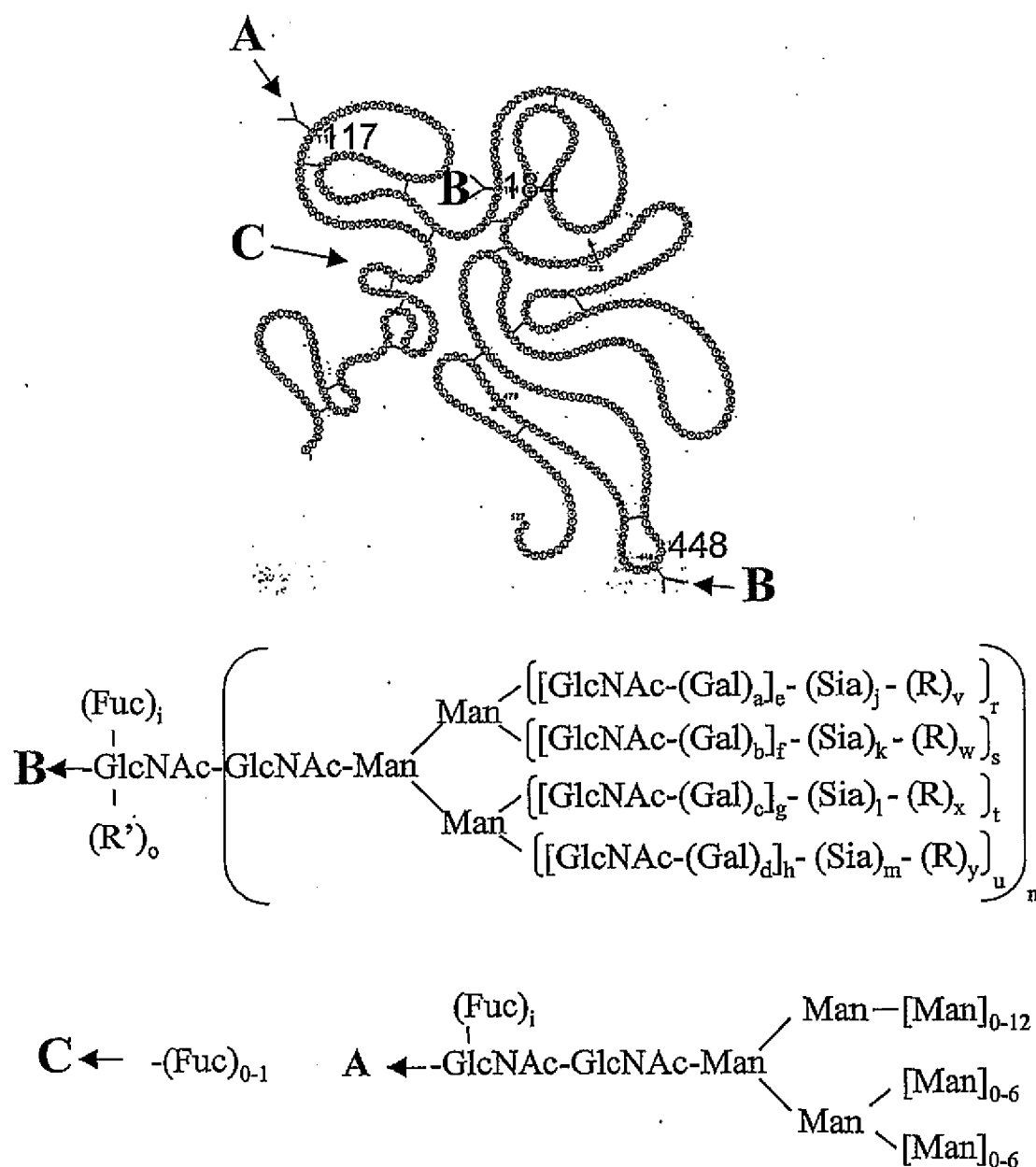
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 37K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 38A

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CHO, BHK, 293 cells, Vero expressed tPA

a-g, n = 1; h = 1 to 3;

j-m, i, (independently selected) = 0 or 1;

r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;

i, r-u (independently selected) = 0 or 1;

o = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG

FIG. 38B

Insect or fungi cell expressed tPA

A = B; a-d, f, h, j-o, s, u, v-y = 0;

e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;

a, c, e, g, i, r, t (independently selected) = 0 or 1;

n = 1; j, l, v, x (independently selected) = 0 or 1;

R = PEG.

FIG. 38C

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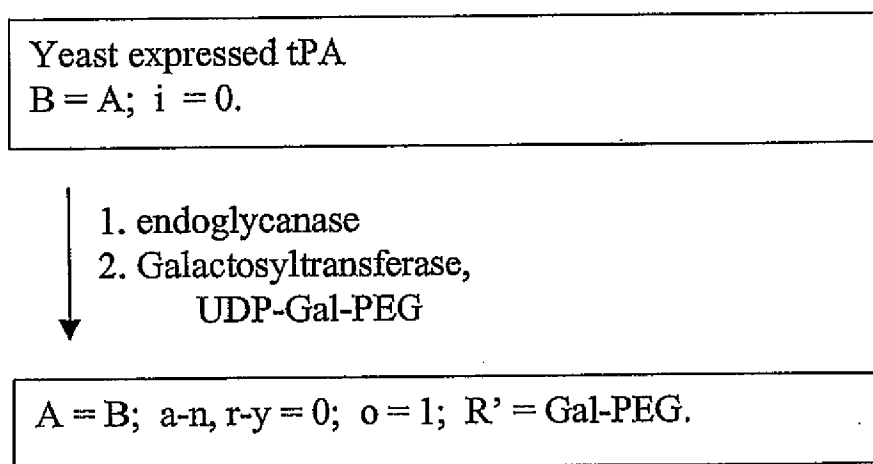


FIG. 38D

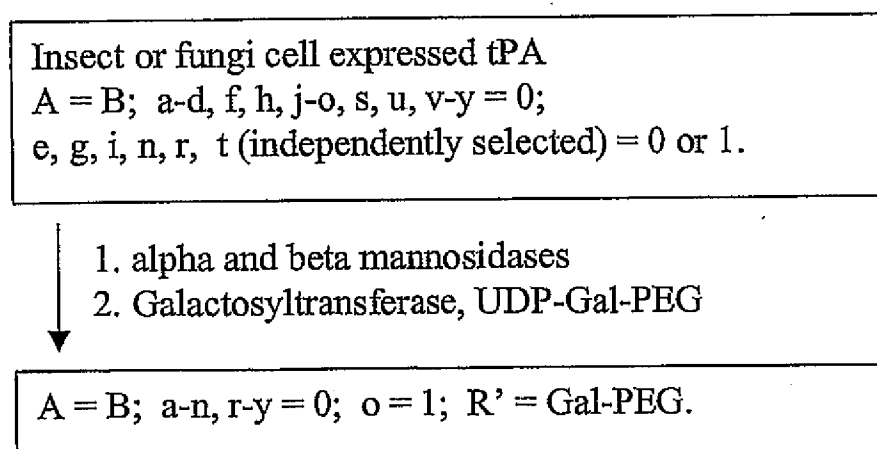


FIG. 38E

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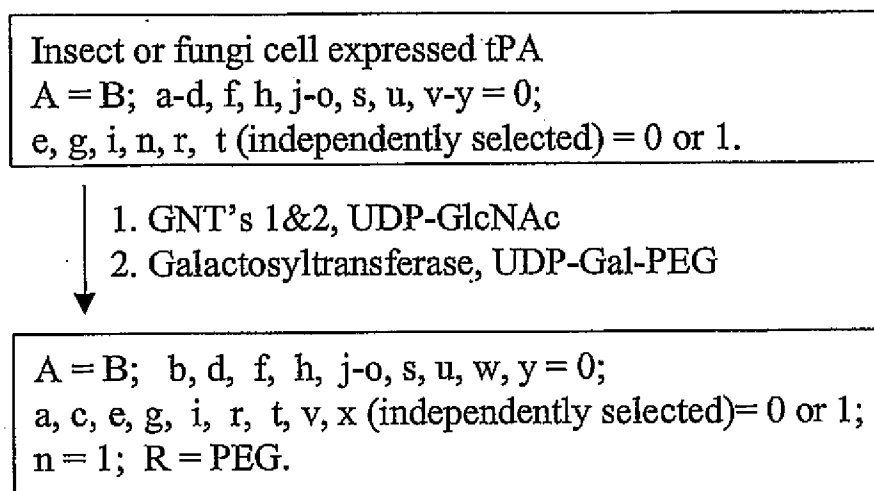


FIG. 38F

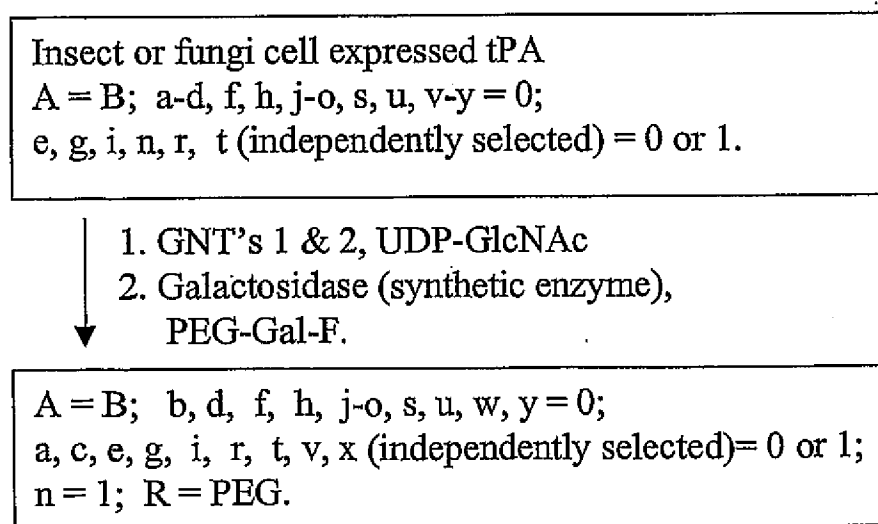
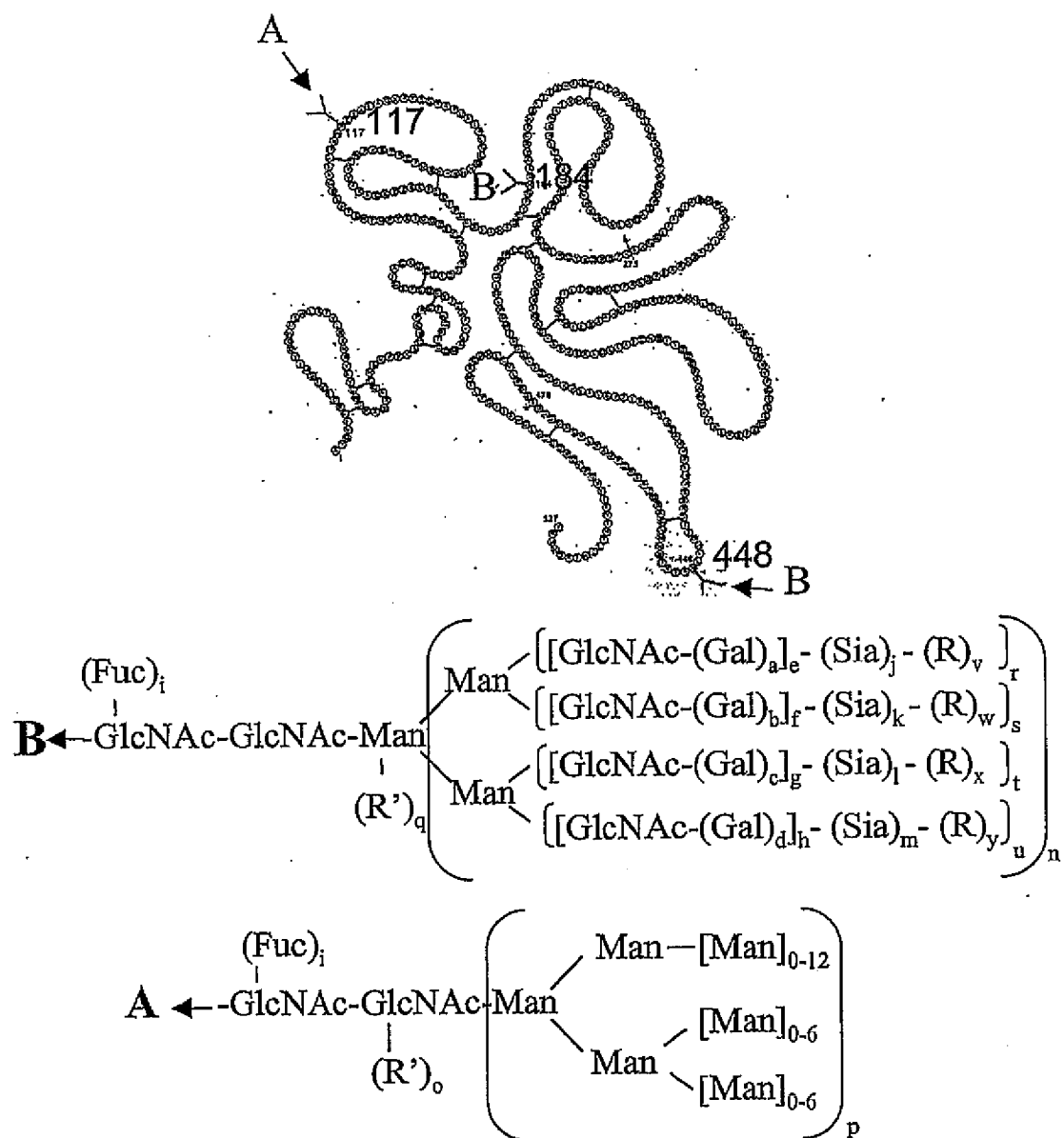


FIG. 38G

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a-d, i, n-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 4.
 j-m (independently selected) = 0 to 20.
 R = polymer; R' = sugar, glycoconjugate.

FIG. 38H

151/345

NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;
n = 1; o, p, q, v-y = 0

- ↓
1. sialidase, alpha-galactosidase
 2. CMP-SA-levulinate, ST3Gal3,
 3. H₄N₂-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;
n = 1; o, p, q = 0;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 38I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;
j-m, i, (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1; q, o, v-y = 0.

- ↓
1. alpha and beta Mannosidases
 2. CMP-SA, ST3Gal3
 3. Galactosyltransferase, UDP-Gal-PEG

a-g, n = 1; h = 1 to 3;
i, r-u (independently selected) = 0 or 1; o = 1;
q, p, v-y = 0; j-m (independently selected) = 0 or 1;
R' = Gal-PEG

FIG. 38J

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Plant expressed tPA

A = B; a-d, f, h, j- m, s, u , v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n=1; R' = xylose

- ↓
1. hexosaminidase,
 2. alpha mannosidase and
xylosidase
 3. GlcNAc transferase, UDP-
GlcNAc-PEG

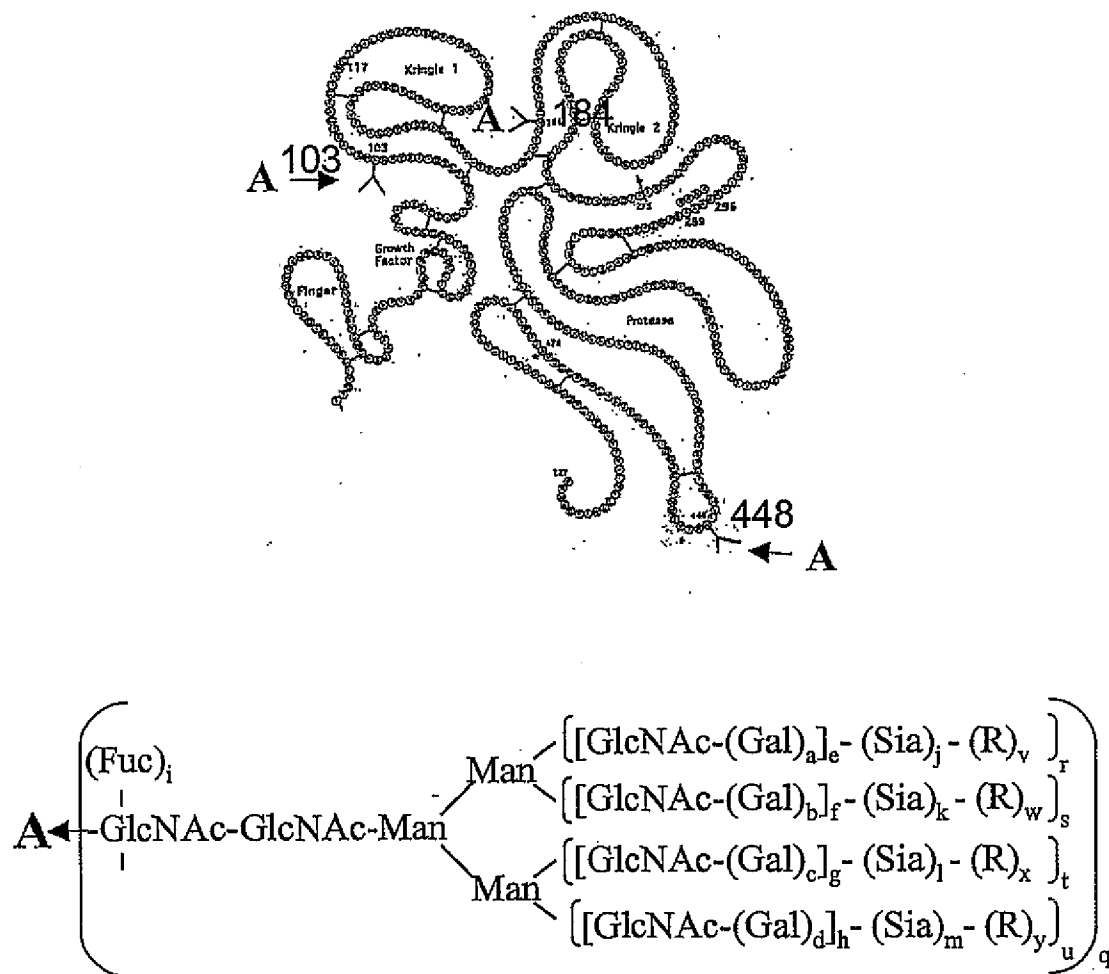
A = B; a-d, f, h, j-n, s, u , v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 38K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 38L

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 38M

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38N

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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

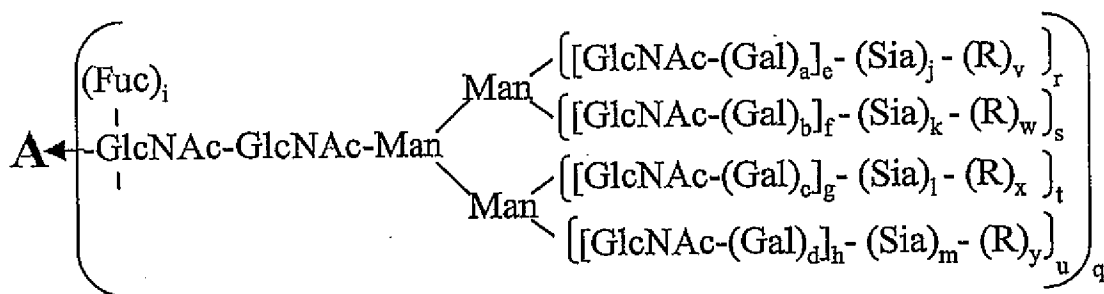
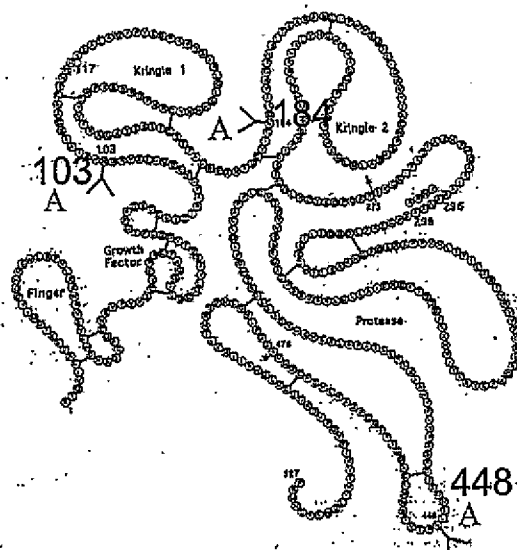
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 380

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a-d, i, q-u (independently selected) = 0 or 1.
e-h (independently selected) = 0 to 6.
j-m (independently selected) = 0 to 100.
v-y = 0; R = polymer.

FIG. 38P

157/345

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38Q

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38R

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

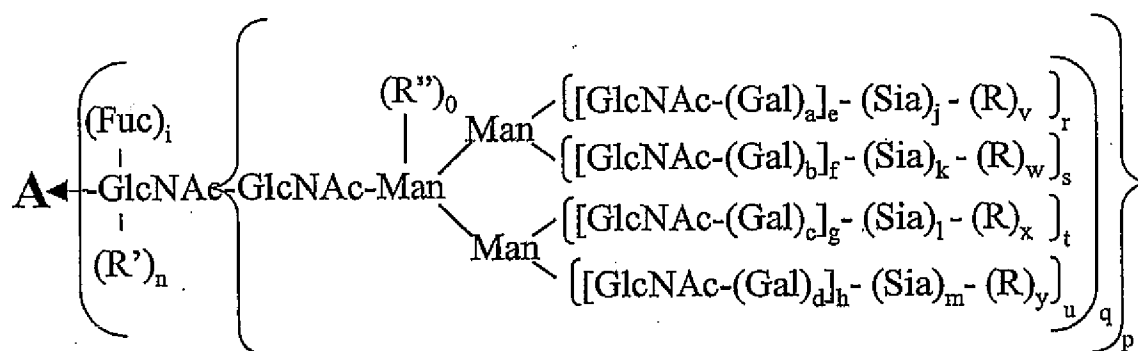
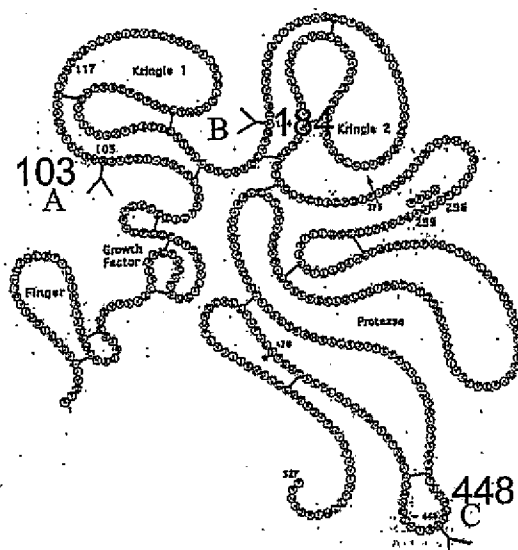


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 38S

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a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 38T

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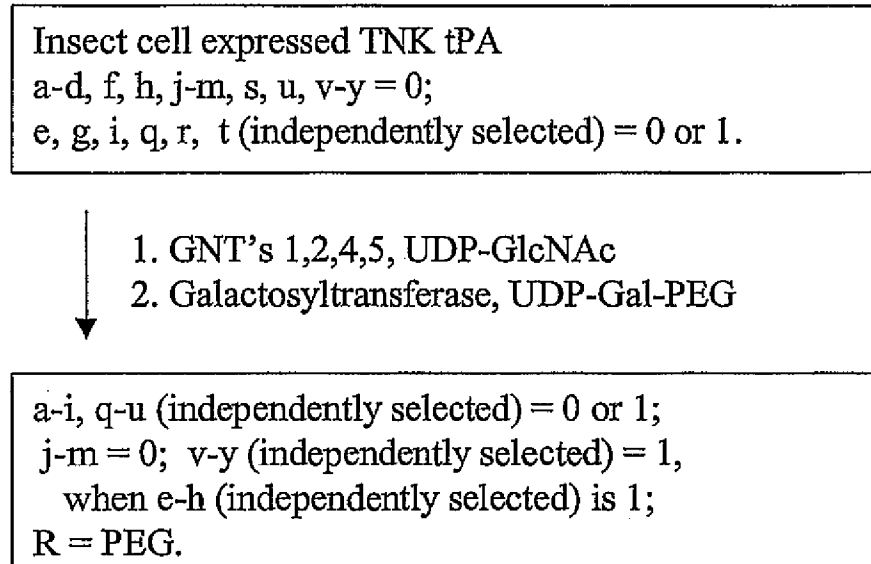


FIG. 38U

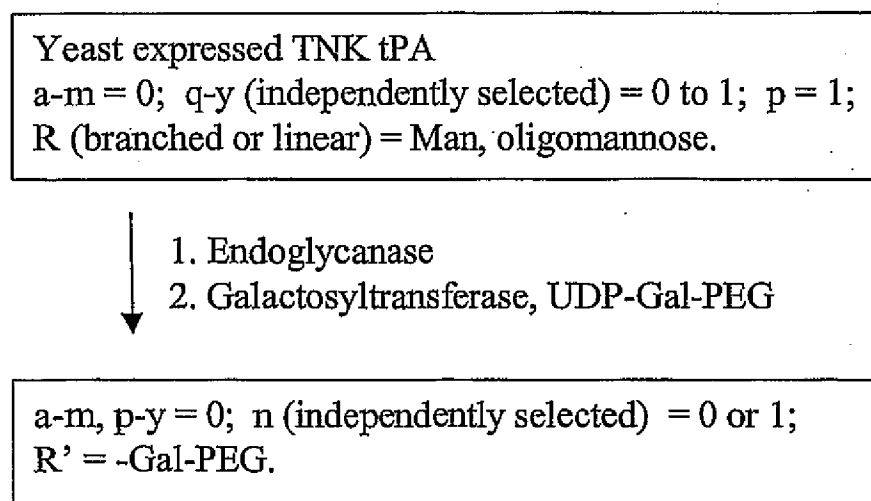


FIG. 38V

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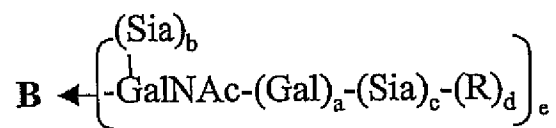
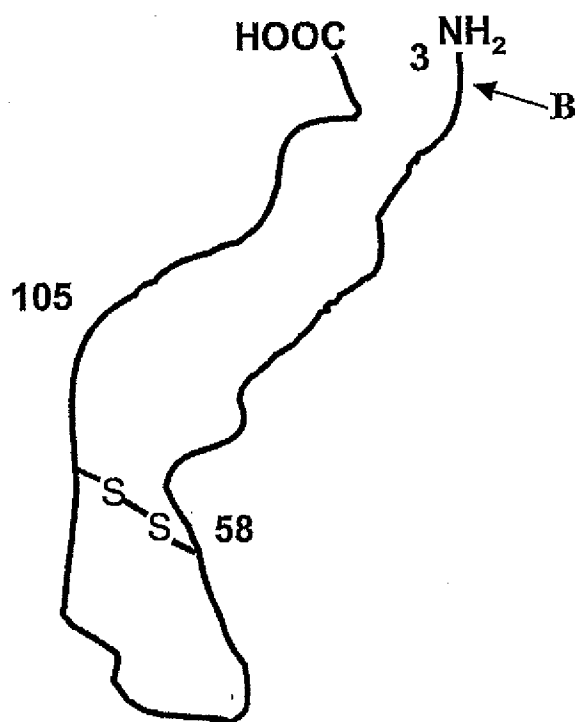
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 38W

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a-c, e (independently selected) = 0 or 1;
 d = 0;
 R = modifying group, mannose, oligo-
 mannose.

FIG. 39A

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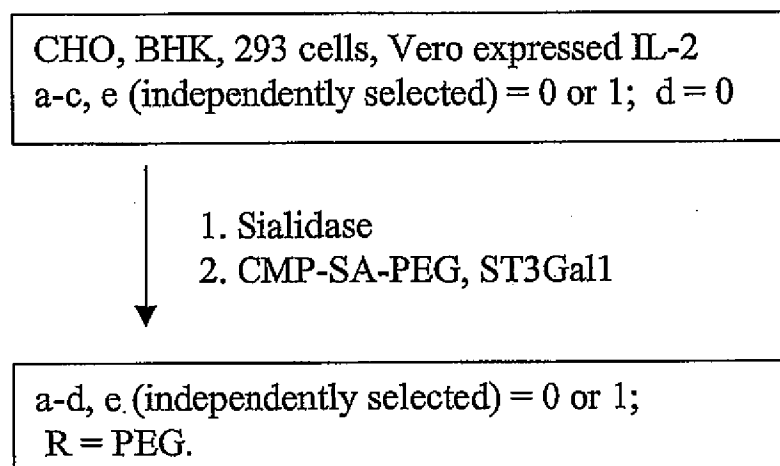


FIG. 39B

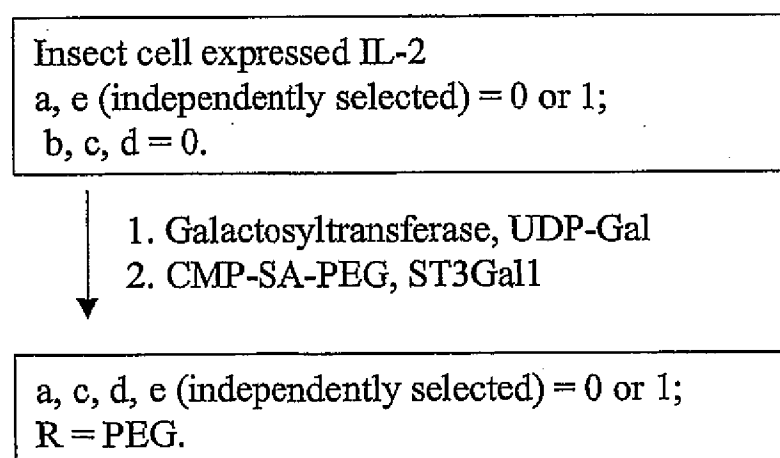


FIG. 39C

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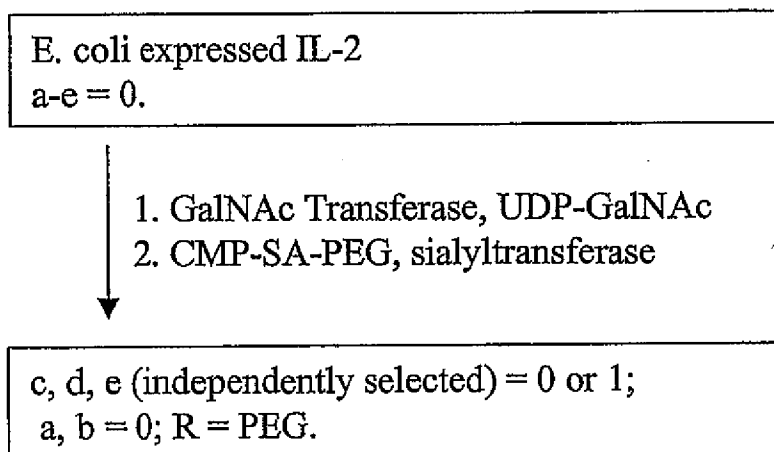


FIG. 39D

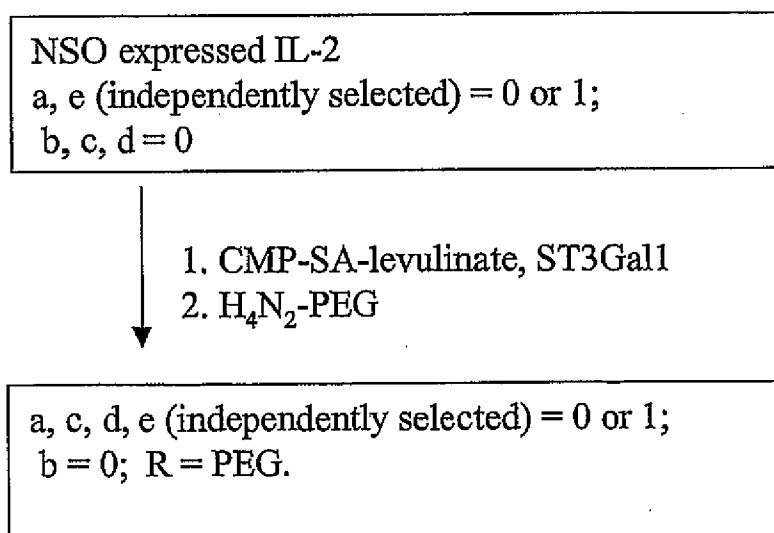


FIG. 39E

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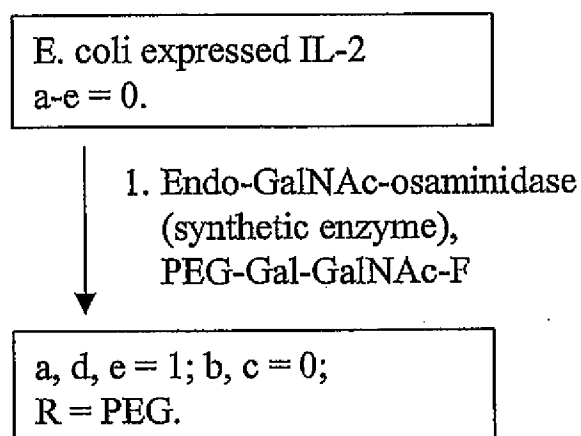


FIG. 39F

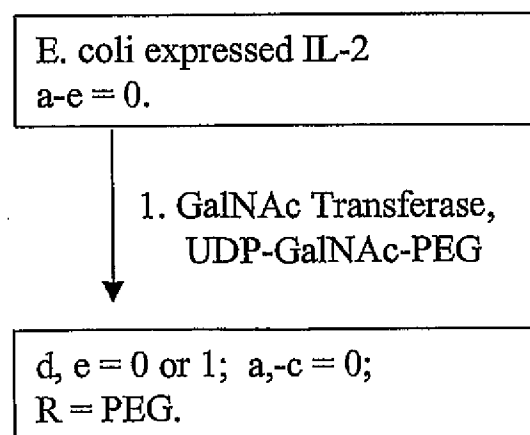
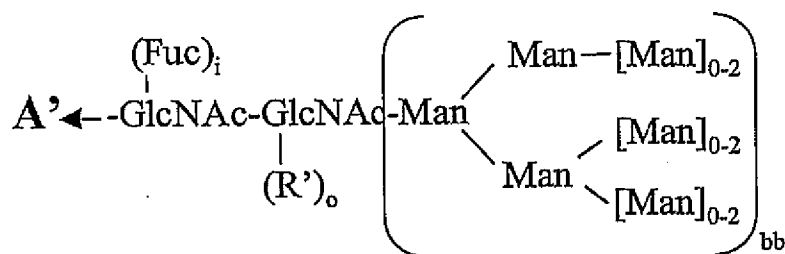
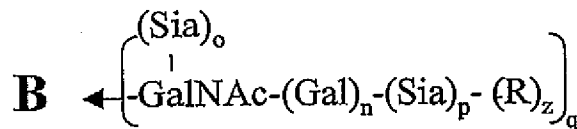
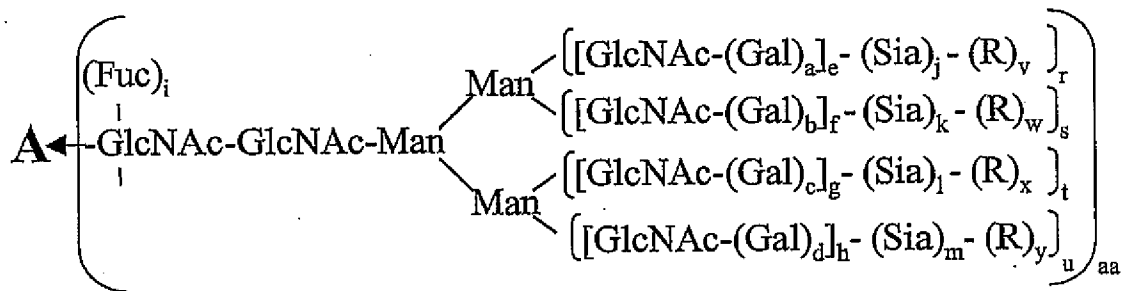


FIG. 39G

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2 peptides
 A and A' - N-linked sites
 B - O-linked sites



Alternate structure
 for some N-linked
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.

aa, bb (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer, glycoconjugate.

FIG. 40A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3
 3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40C

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CHO, BHK, 293s cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;
v-z = 0.

↓
1. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40D

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected) 0 or 1;
v-z = 0.

↓
1. CMP-SA-PEG, ST3Gal1

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40E

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

when j-m (independently selected) is 2;

R = PEG.

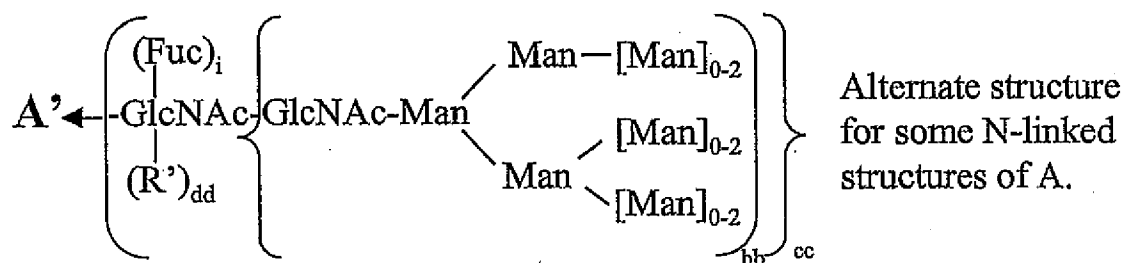
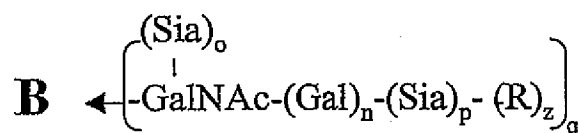
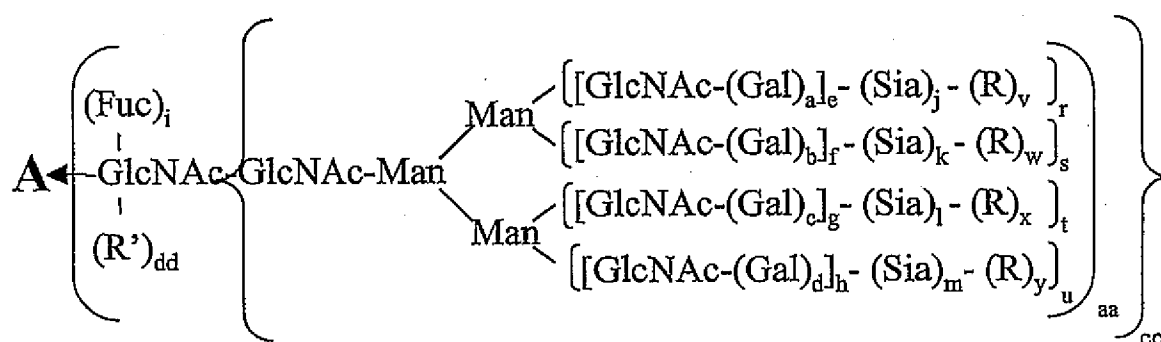
FIG. 40F

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2 peptides

A or A' - N-linked sites

B - O-linked sites



a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

$$y-z = 0;$$

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 40G

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. CMP-SA-levulinate, ST3Gal3,
2. H₄N₂-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. endo-H
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40I

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
 2. endo-H
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40J

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 40K

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

1. mannosidases

2. GNT-1, 2, 4 & 5; UDP-GlcNAc

↓ 3. galactosyltransferase, UDP-Gal

4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;

dd, v-z = 0.

FIG. 40L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

1. mannosidases

↓ 2. GNT-1, UDP-GlcNAc-PEG

e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0.

FIG. 40M

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 41B

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 41C

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NSO expressed Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0;
 Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 41D

CHO, BHK, 293 cells, Vero expressed Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ↓ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 41E

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 41F

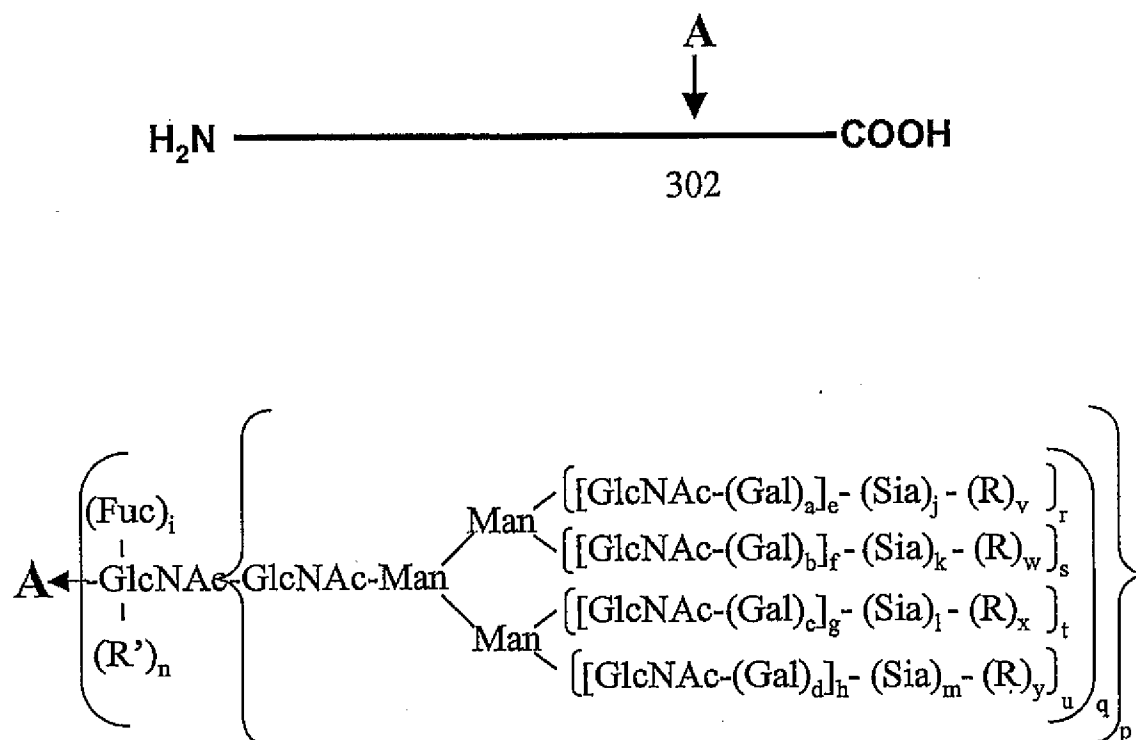
CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 41G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 41H

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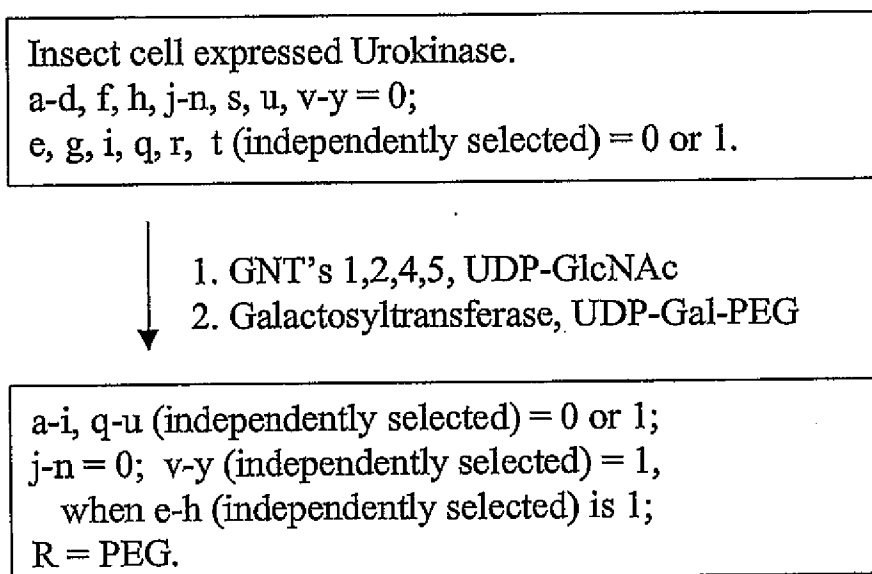


FIG. 41I

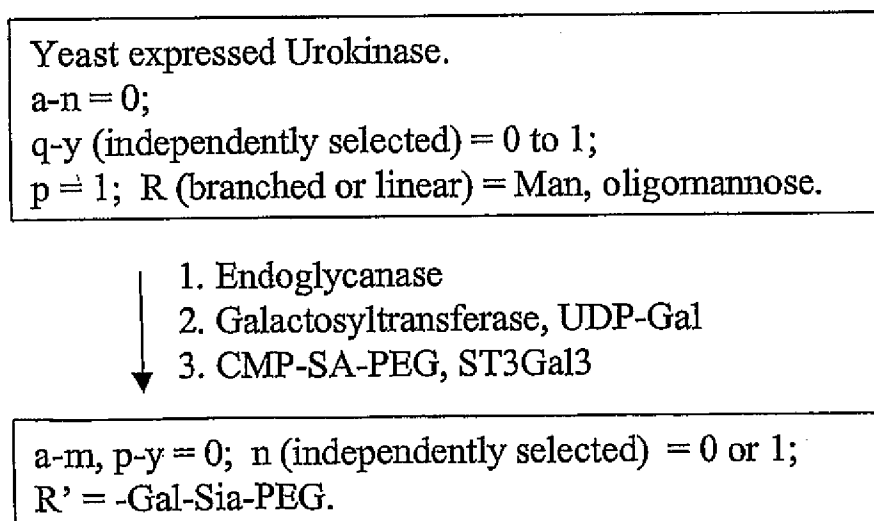


FIG. 41J

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CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated Urokinase produced in CHO.
 - ↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 41K

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
 2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 41L

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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

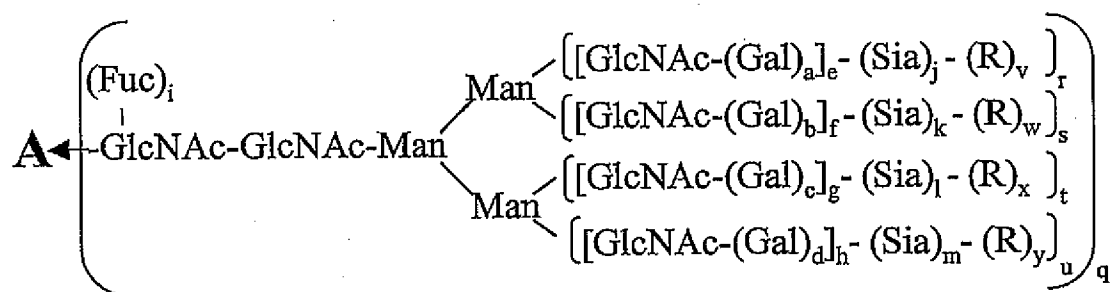
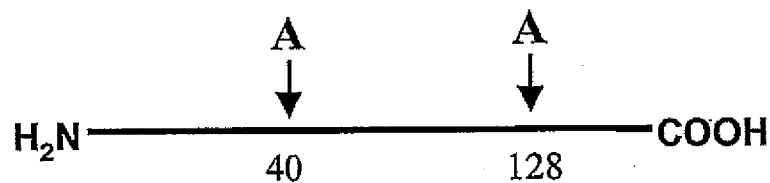
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 41M

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 42B

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42C

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NSO expressed DNase I.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 42D

CHO, BHK, 293 cells, Vero expressed DNase I.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq), ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42E

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42F

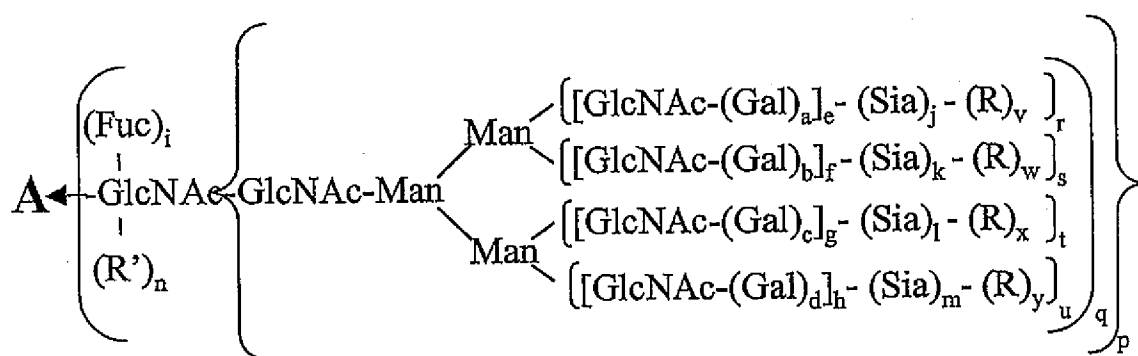
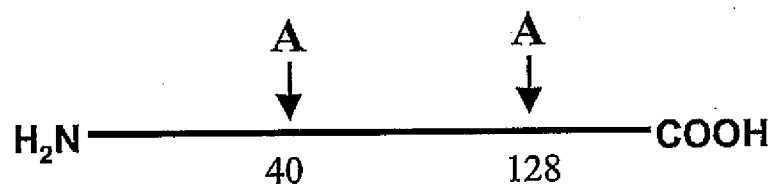
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 42G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

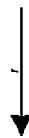
FIG. 42H

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Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y' = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 42I

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 42J

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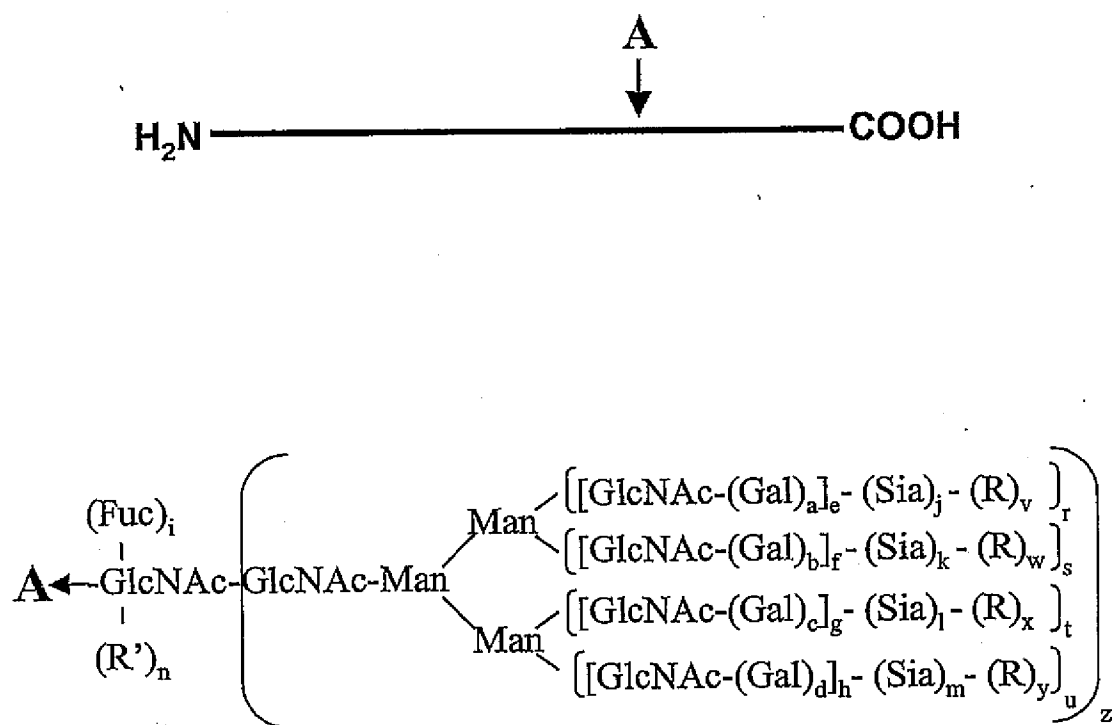
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 42K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 43A

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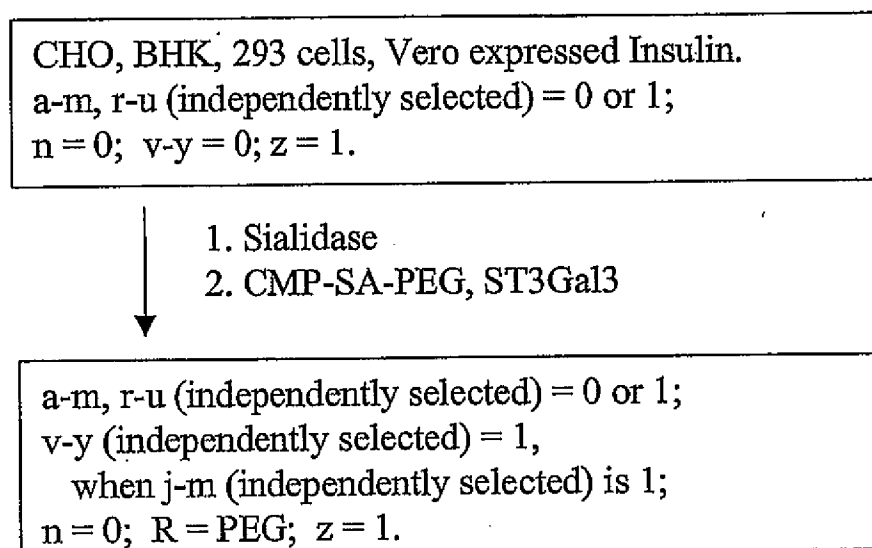


FIG. 43B

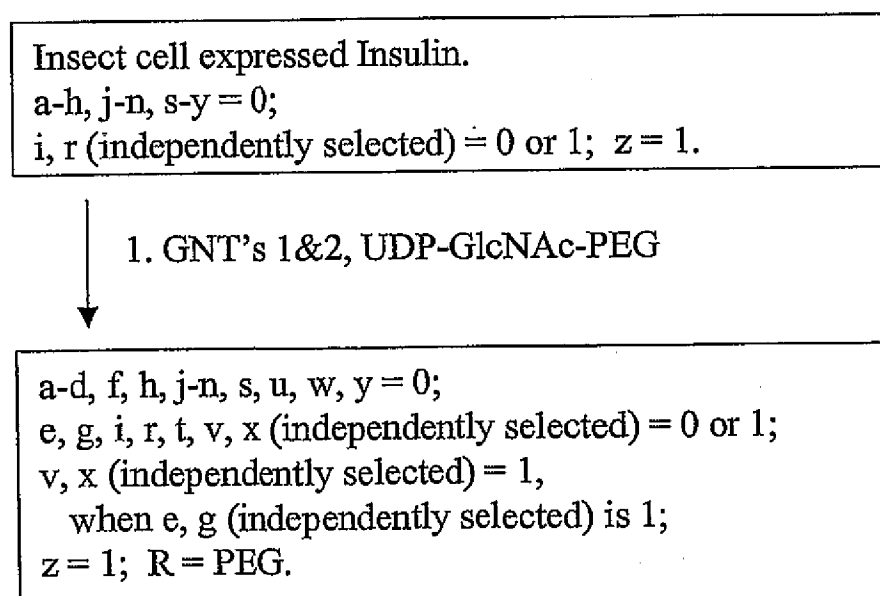


FIG. 43C

191/345

Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;
z = 1;

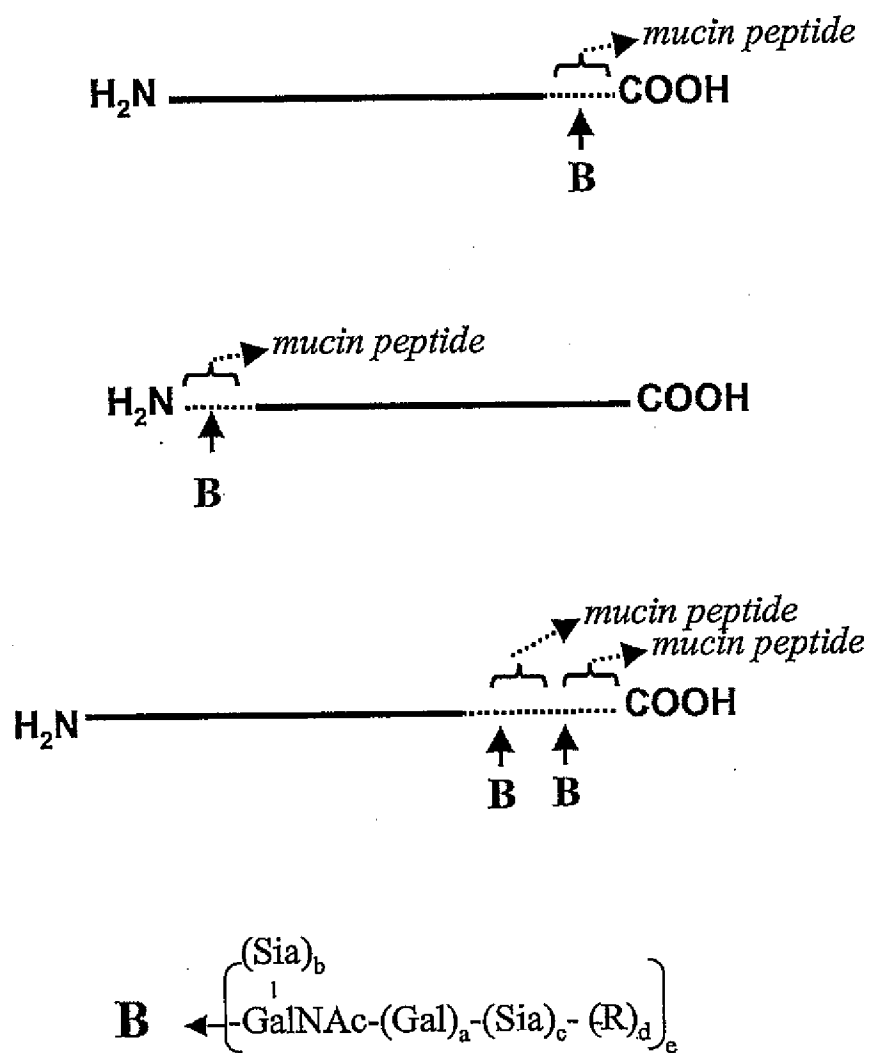
R (branched or linear) = Man, oligomannose or
polysaccharide.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 43D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 43E

193/345

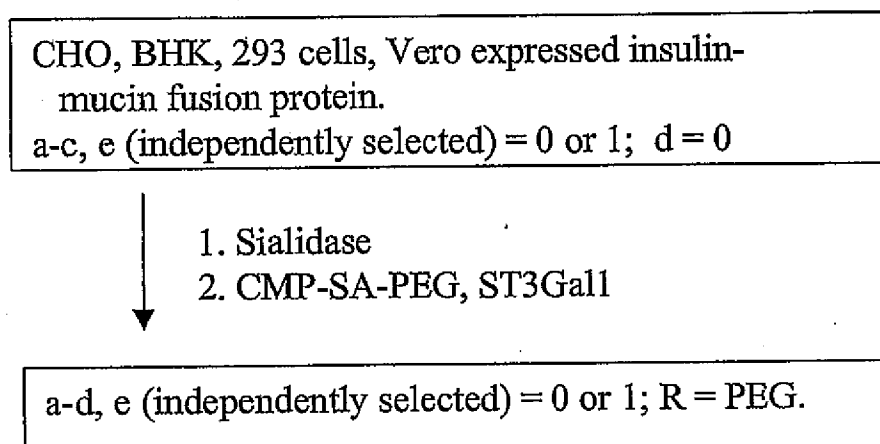


FIG. 43F

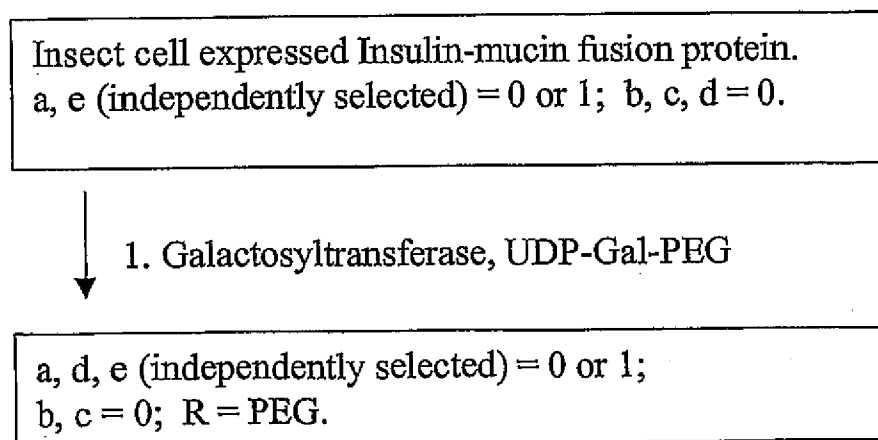


FIG. 43G

194/345

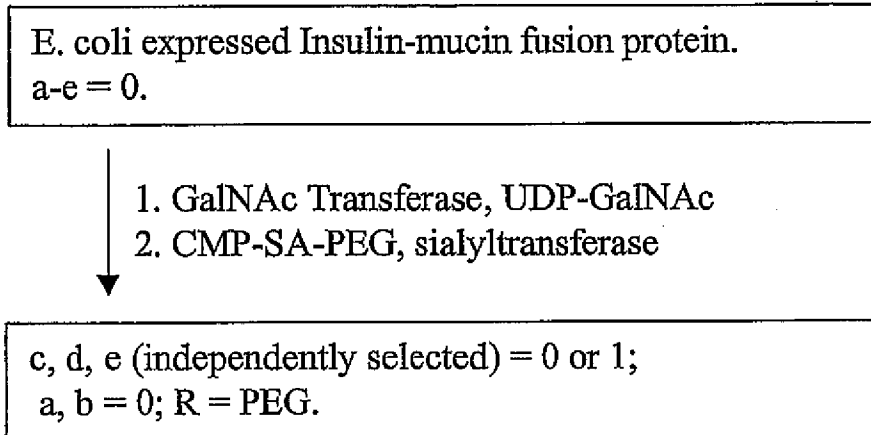
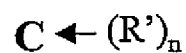
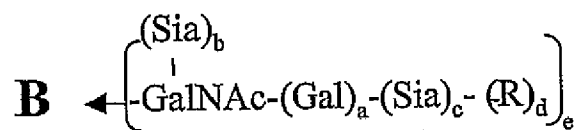
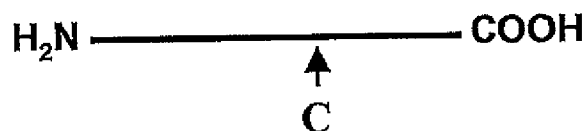
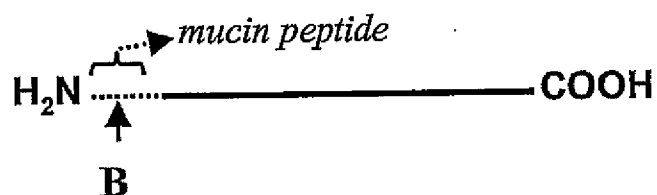
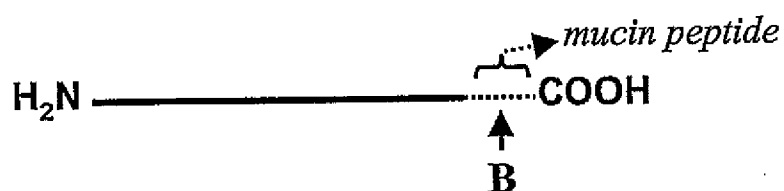


FIG. 43H

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 43I

196/345

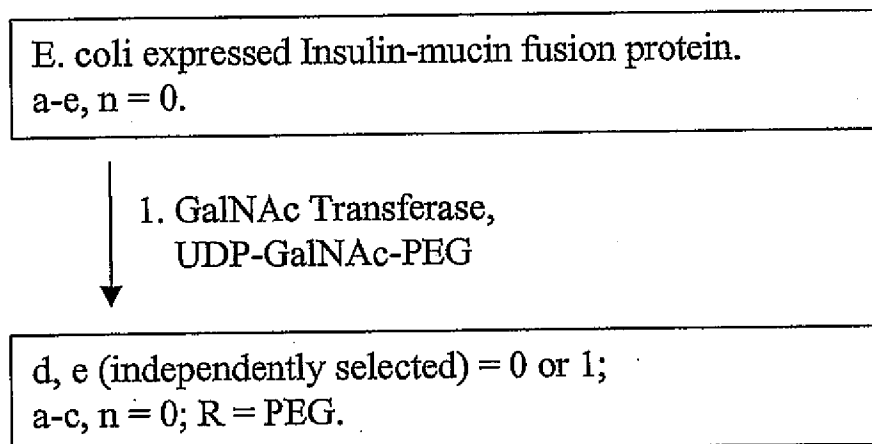


FIG. 43J

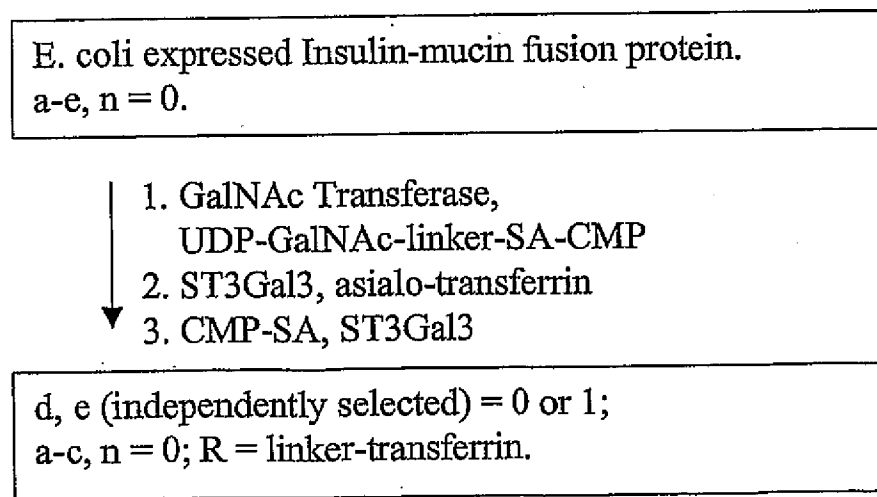


FIG. 43K

197/345

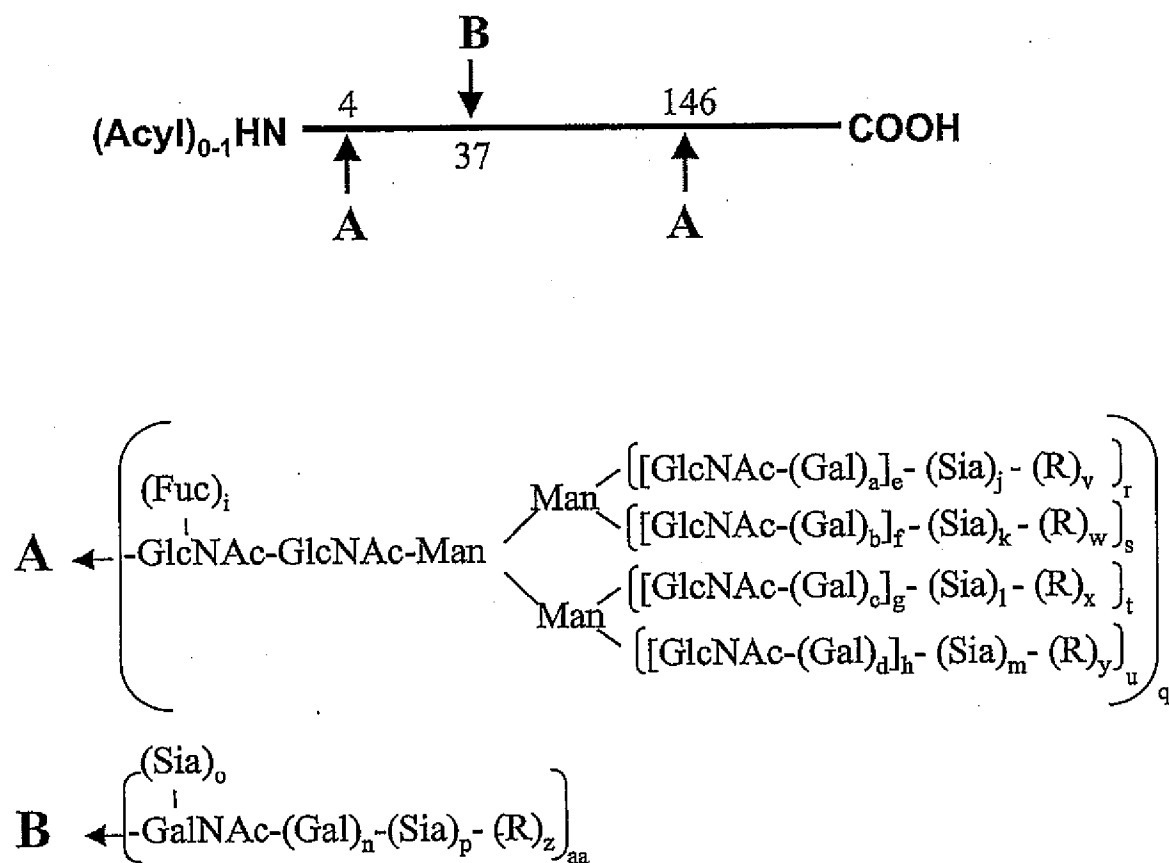
E. coli expressed Insulin (N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1;
R' = linker-transferrin.

FIG. 43L

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a-d, i, n-u, aa (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

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CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-linker-lipid-A,
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
o, p, z = 0; n, e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = linker-lipid-A.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-linker-tetanus toxin, ST3Gal1
 - ↓ 3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 44C

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NSO expressed M-antigen.

a-d, i-n, o-u, aa (independently selected) = 0 or 1;

e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. α -galactosidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-KLH, ST3Gal1

a-d, i-n, p-u, z, aa (independently selected) = 0 or 1;

e-h = 1; o, v-y = 0;

z = 1, when p = 1;

R = KLH.

FIG. 44D

Yeast expressed M-antigen.

a-p, z = 0; q-y, aa (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. α 1,2-mannosidase
 2. GNT 1,
- ↓ UDP-GlcNAc-linker-diphtheria toxin.

e, q, l, m, r, t, u, v, aa (independently selected) = 0 or 1;

a-d, f-h, j, k, n-p, s, w-z = 0;

Sia = Man; R = linker-diphtheria toxin.

FIG. 44E

201/345

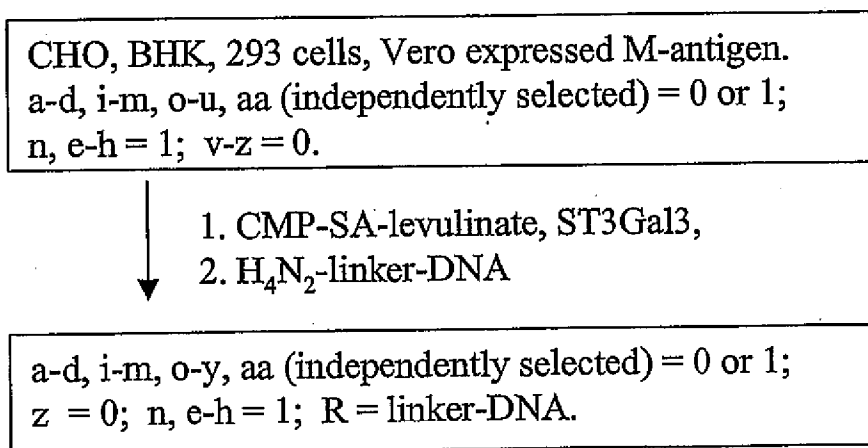


FIG. 44F

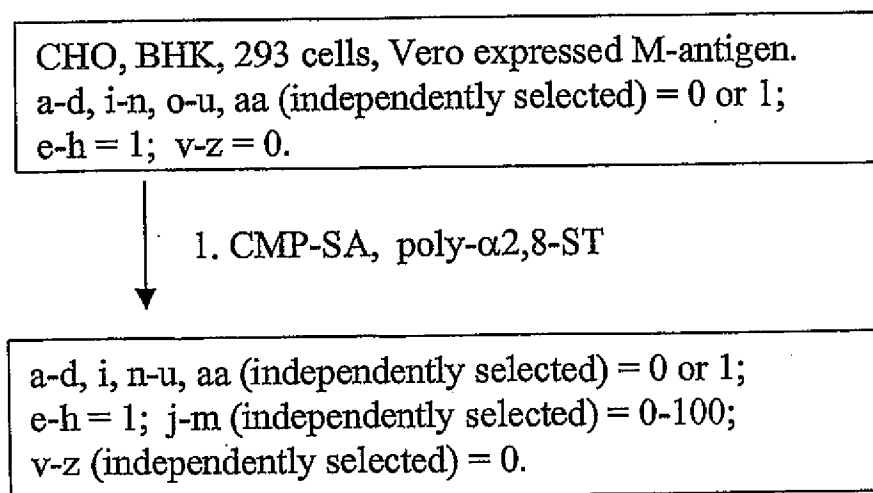
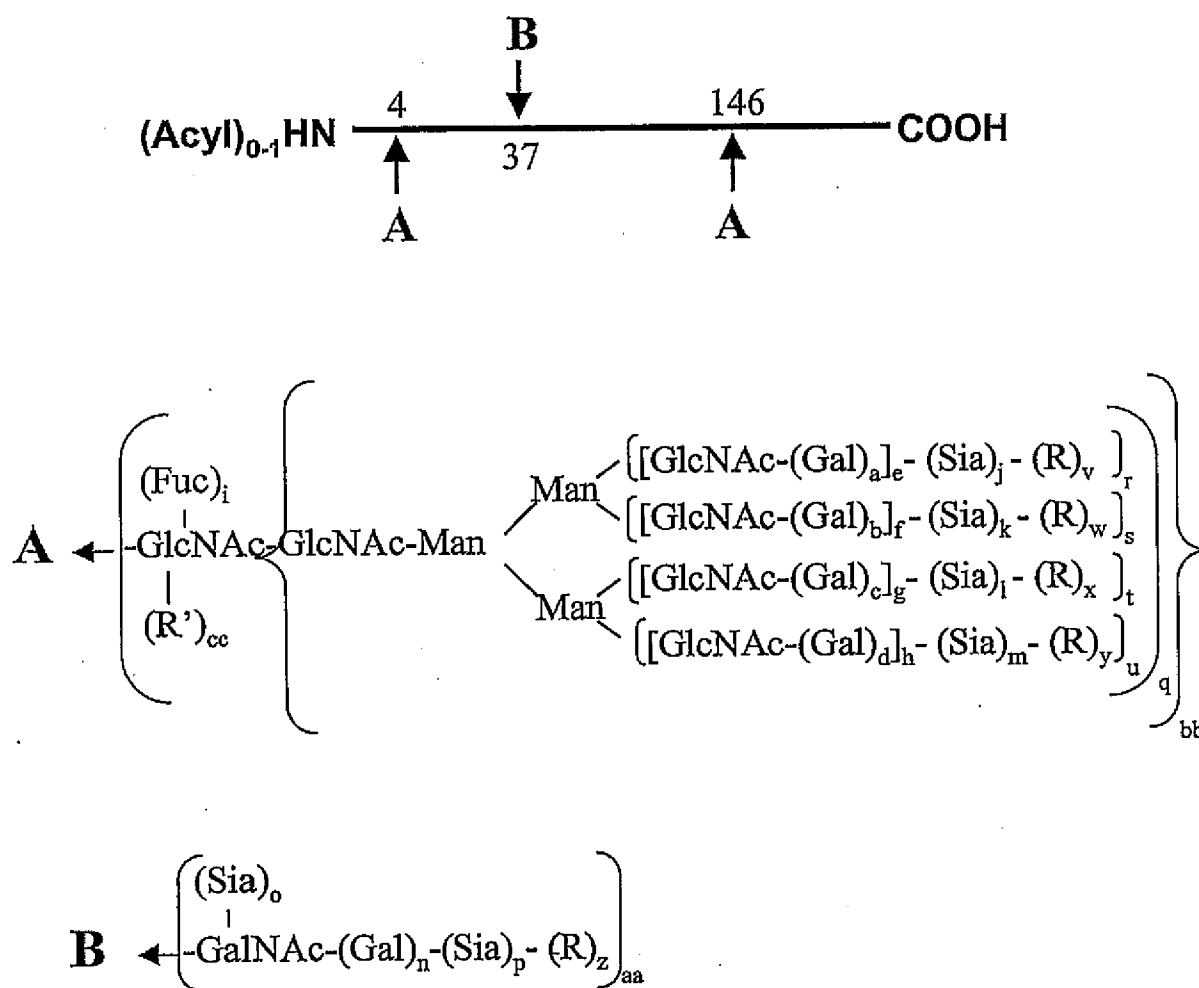


FIG. 44G

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a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 44H

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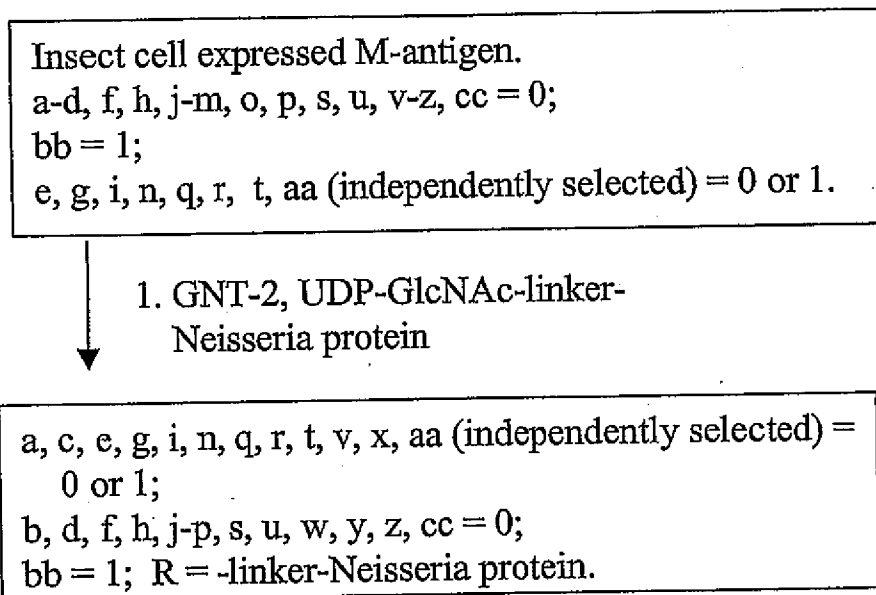


FIG. 44I

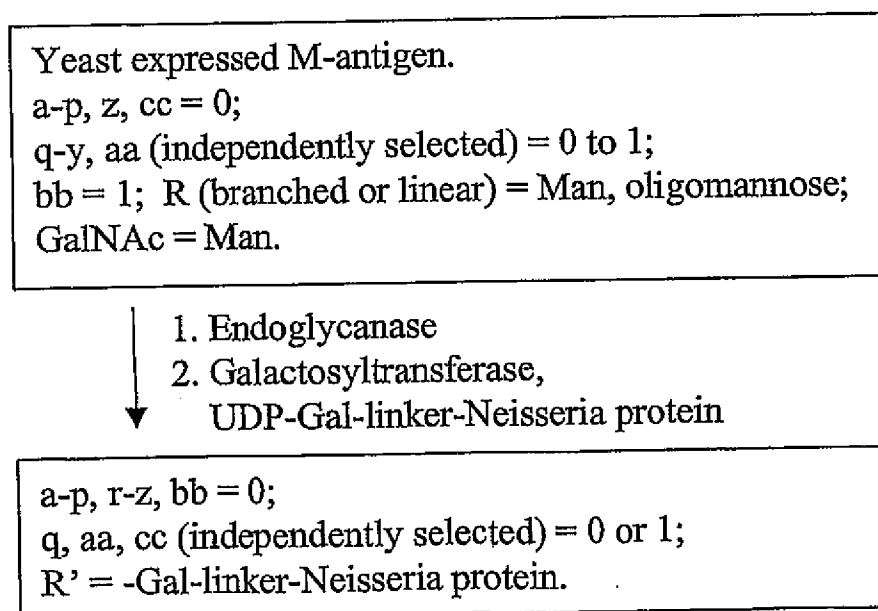


FIG. 44J

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Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

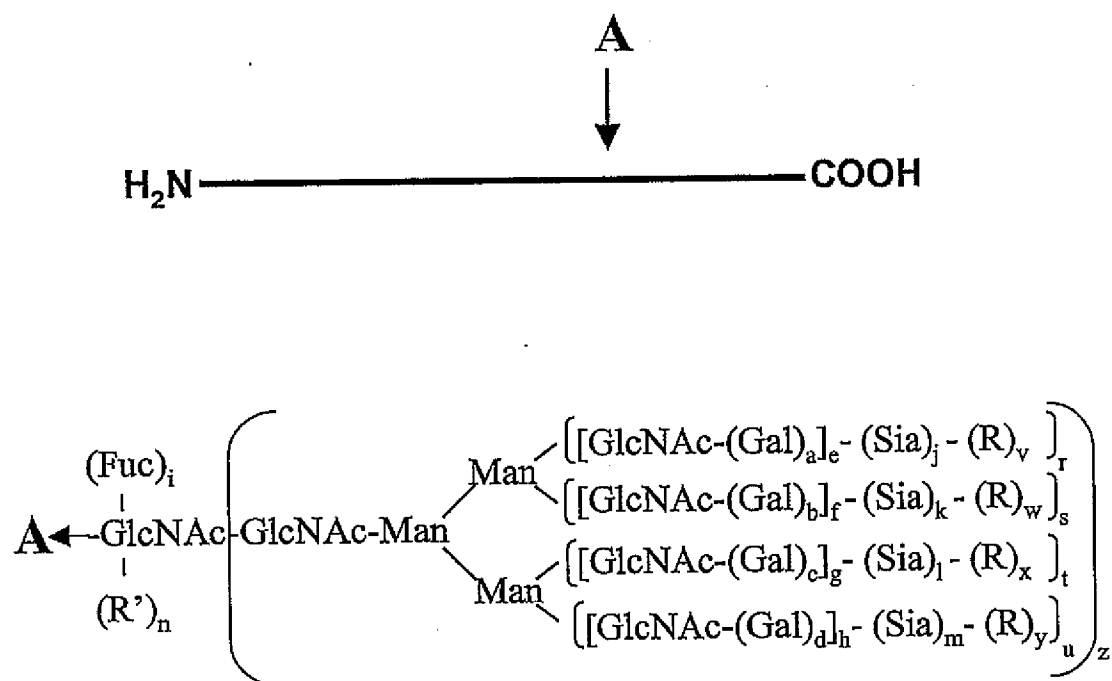
4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 44K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 45A

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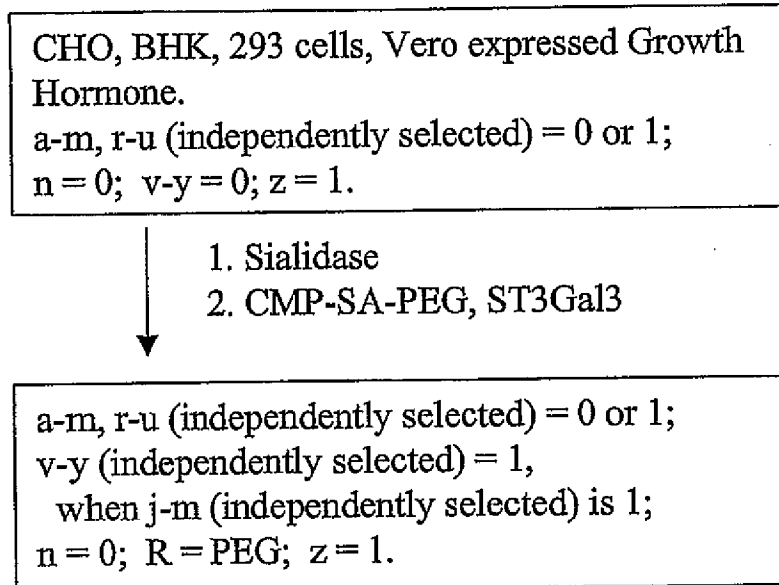


FIG. 45B

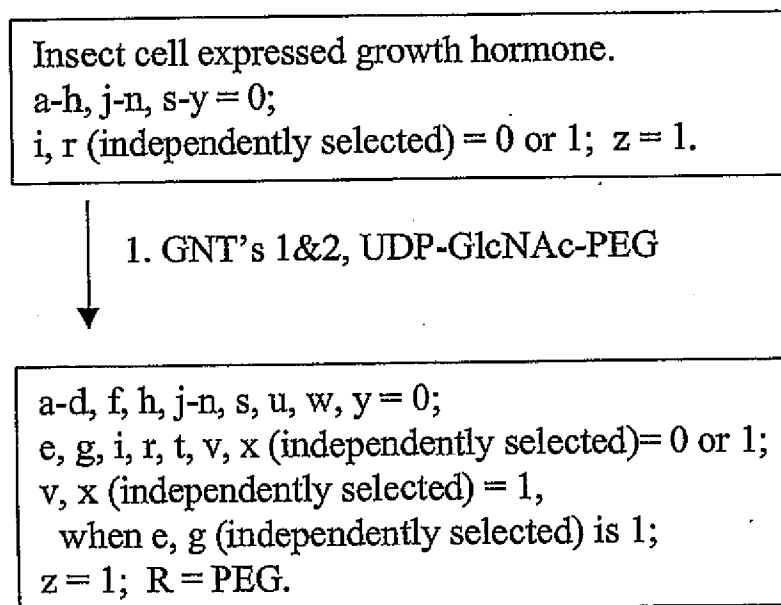


FIG. 45C

207/345

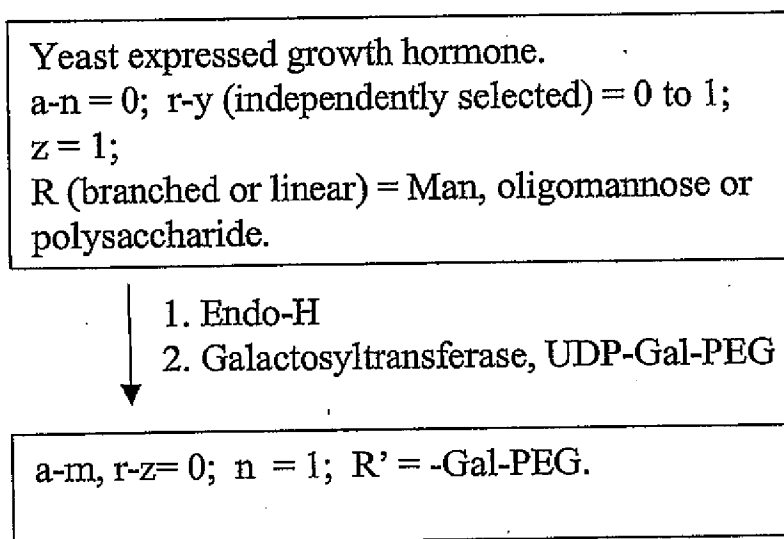
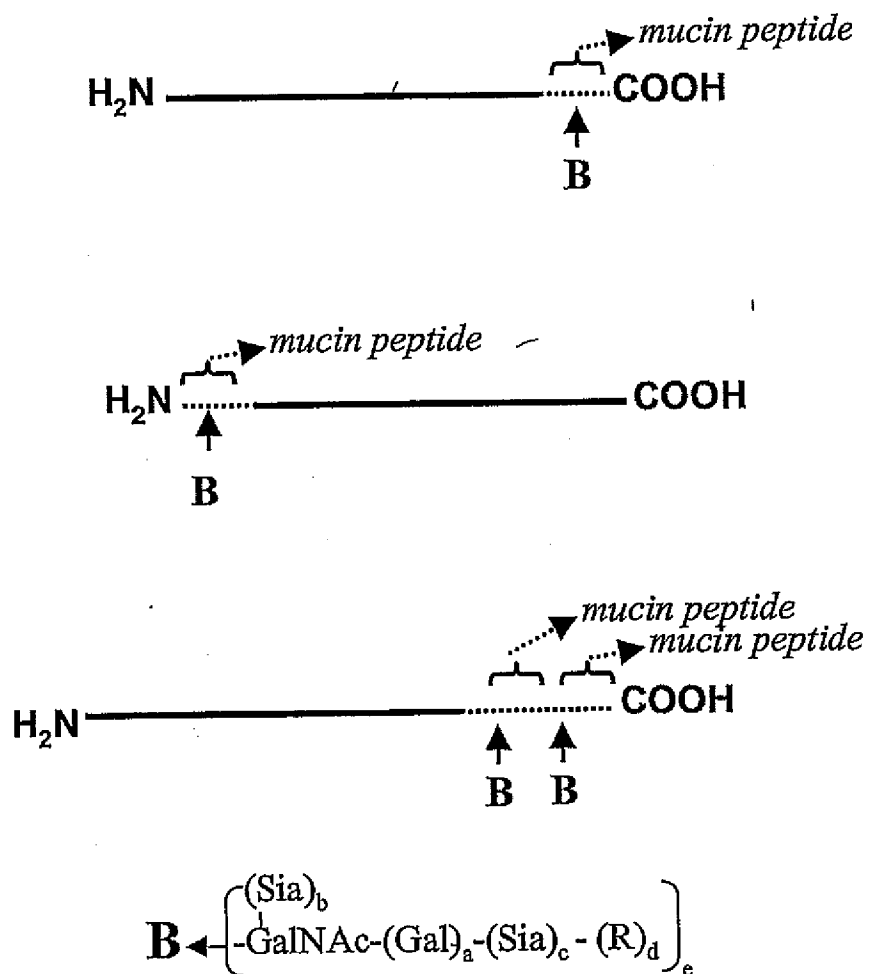


FIG. 45D

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a-c, e (independently selected) = 0 or 1;
 d = 0;
 R = modifying group, mannose, oligo-
 mannose.

FIG. 45E

209/345

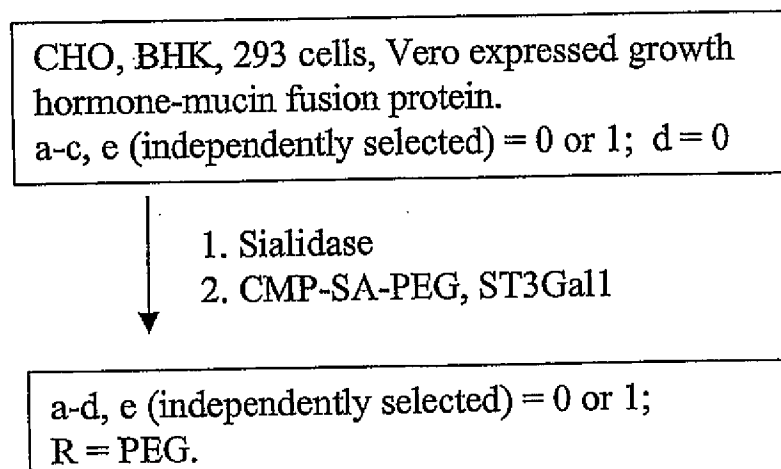


FIG. 45F

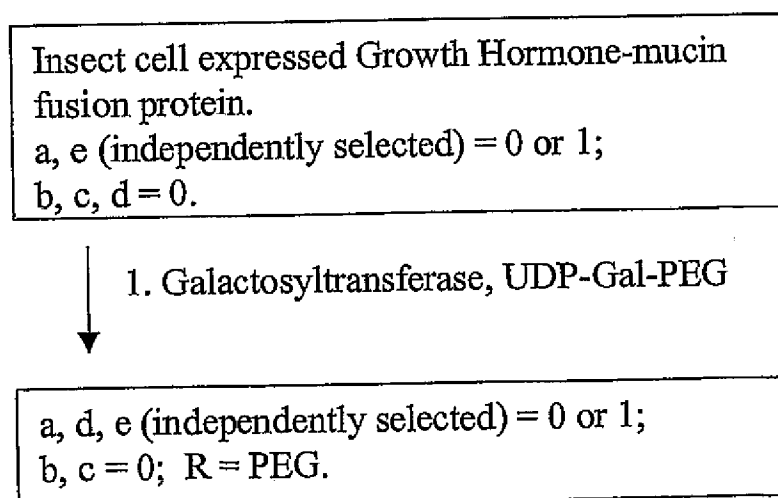


FIG. 45G

210/345

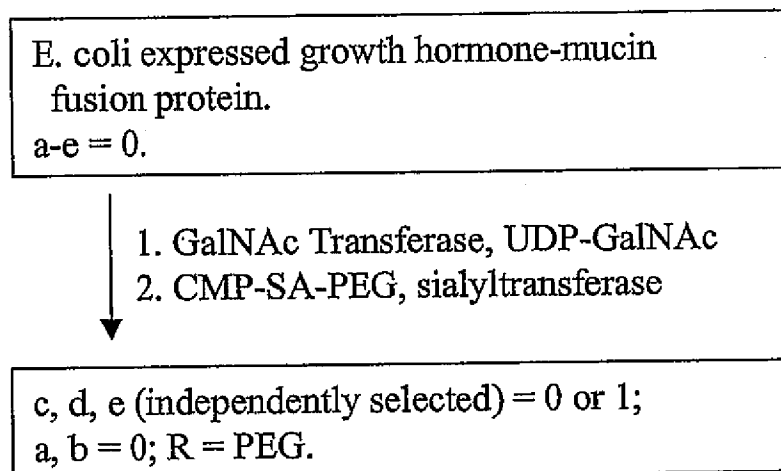


FIG. 45H

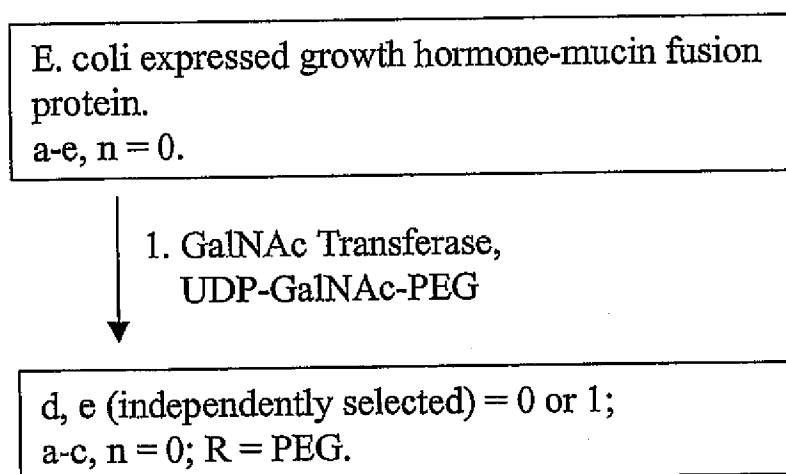


FIG. 45I

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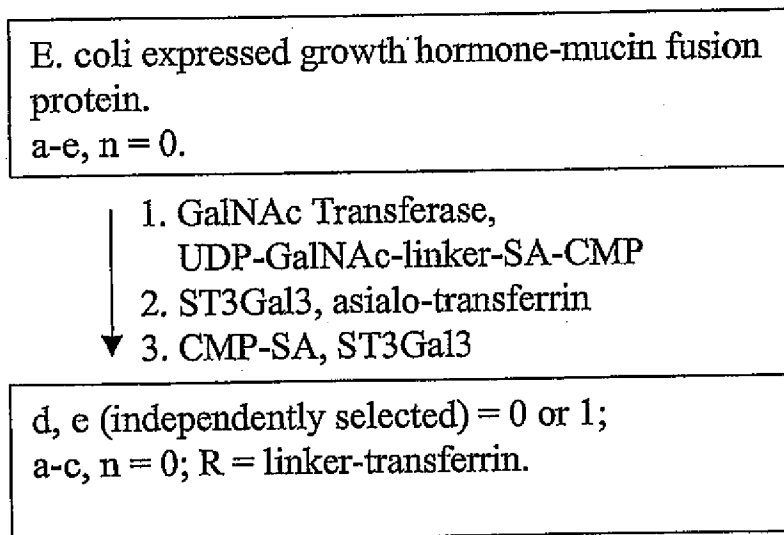


FIG. 45J

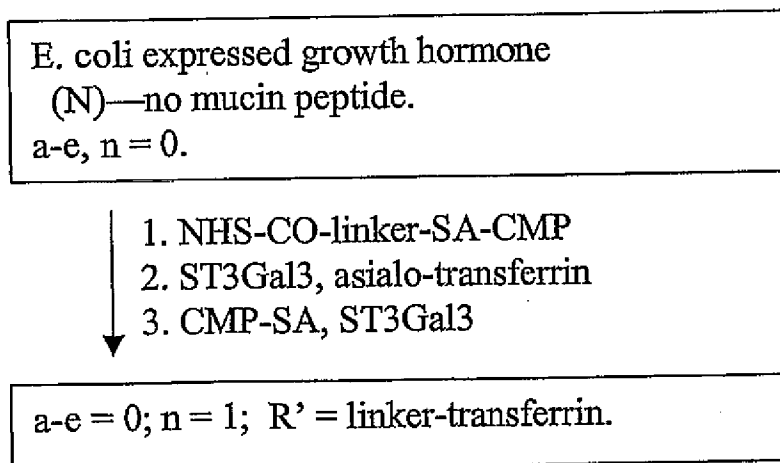
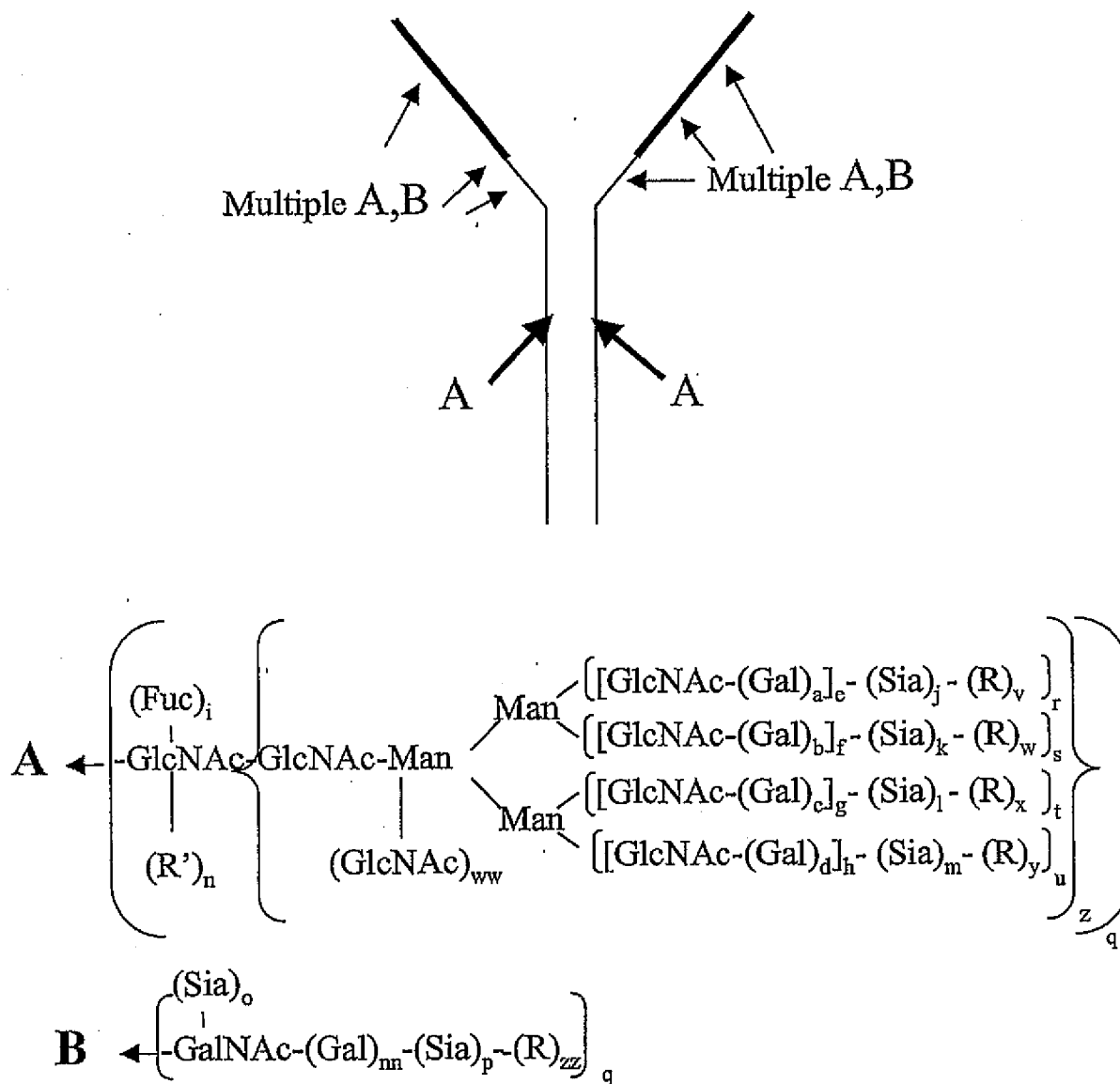


FIG. 45K

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a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46A

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
2. galactosyltransferase, UPD-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 46C

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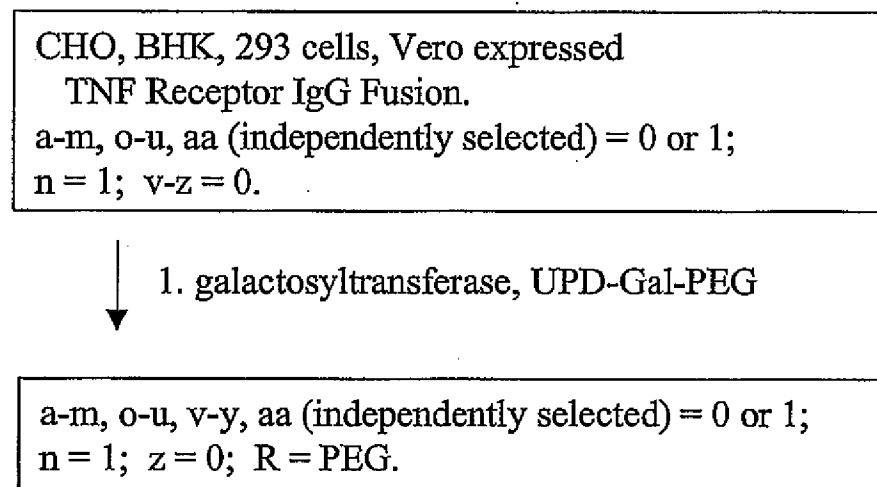


FIG. 46D

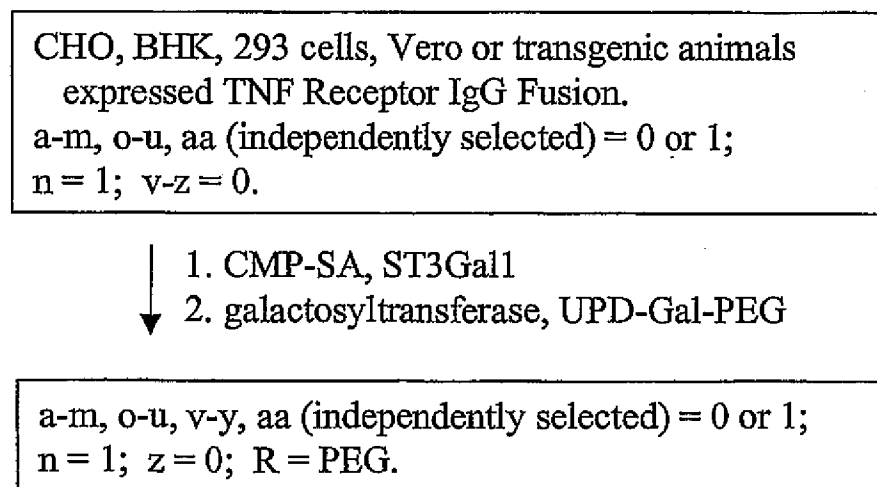


FIG. 46E

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-levulinate, ST3Gal1
2. H₄N₂-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 46F

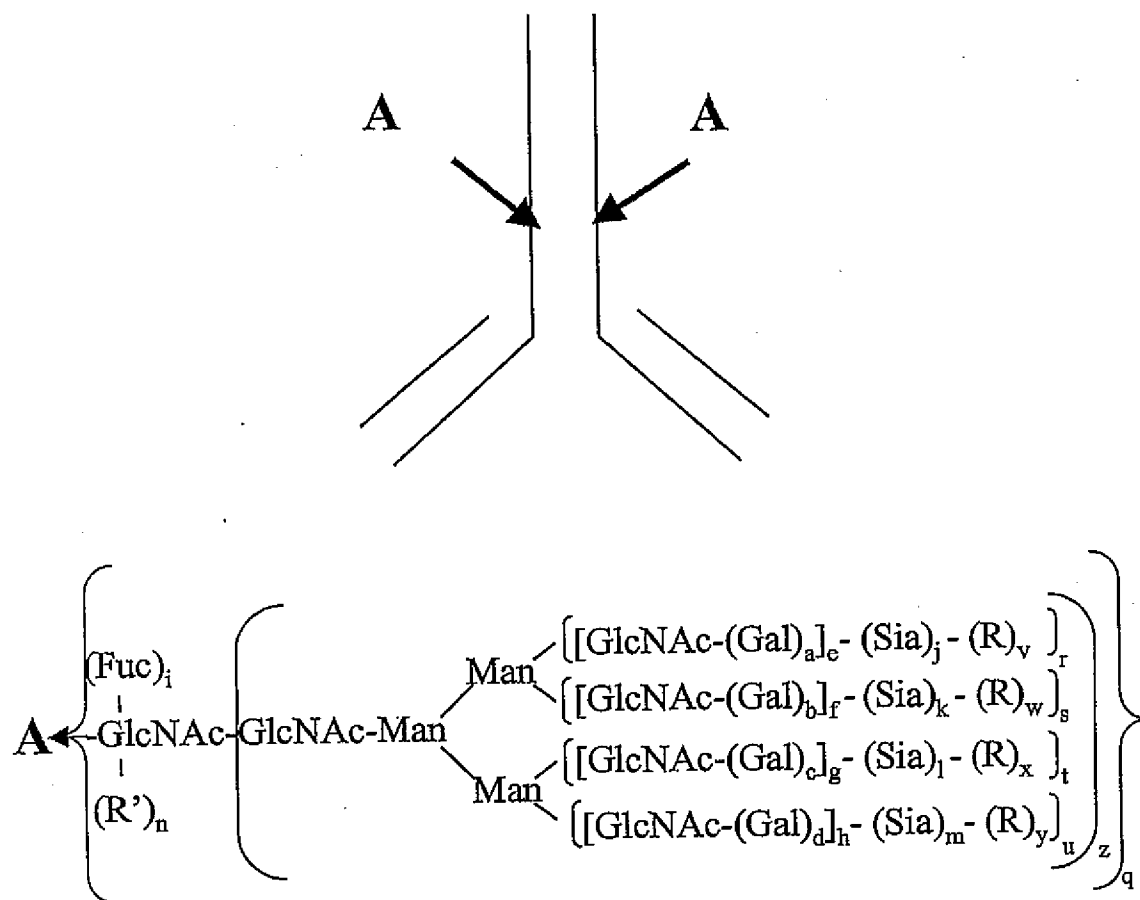
CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-PEG, α 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 46G

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a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-k (independently selected) = 0 or 1.

M = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 47A

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CHO, BHK, 293 cells, Vero expressed Herceptin.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
 e, g, r, t = 1; R = toxin;
 f, h, k, m, n, s, u-y = 0; q, z = 1;
 v-y (independently selected) = 51,
 when j, l (independently selected) is 1.

FIG. 47B

CHO, BHK, 293 cells, Vero or fungal expressed Herceptin.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.



1. galactosyltransferase,
UPD-Gal-Toxin

a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = toxin.

FIG. 47C

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Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

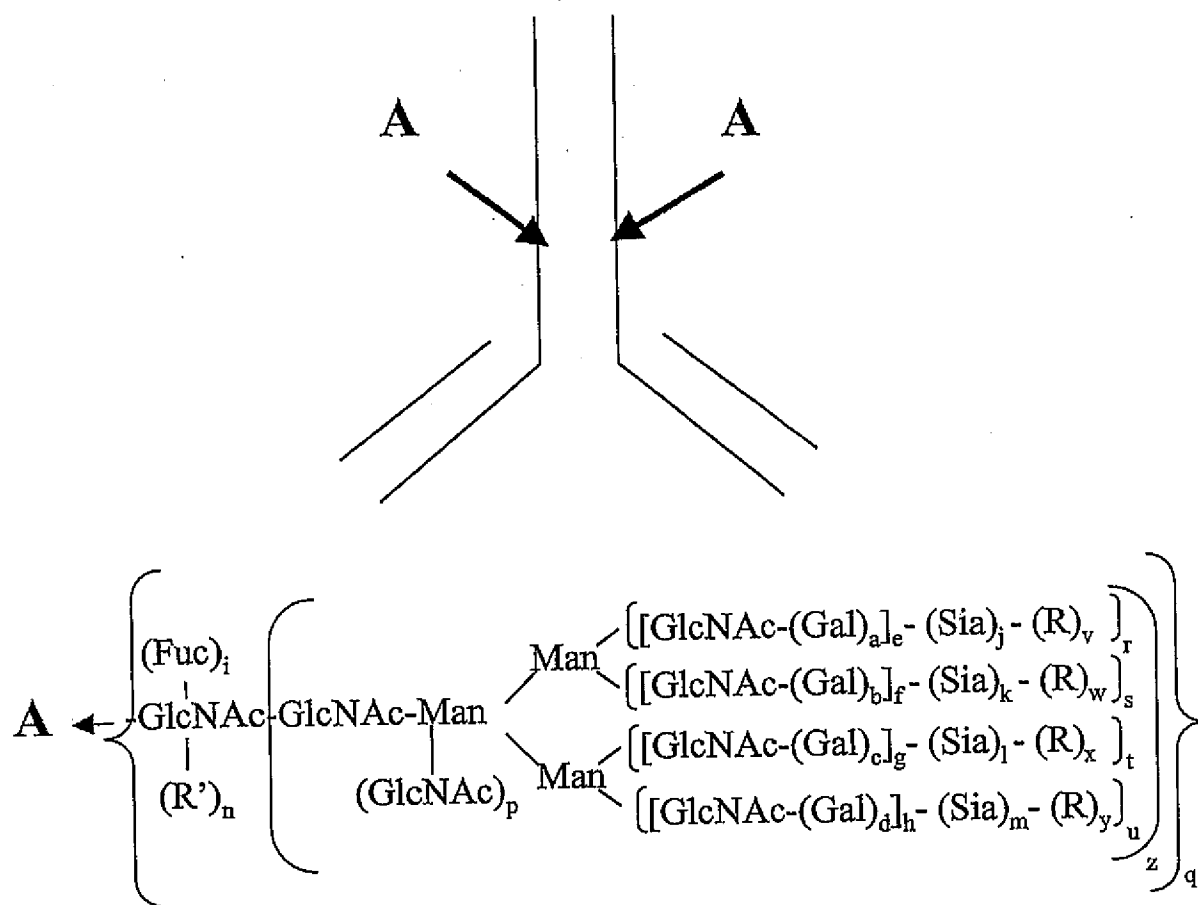
- ↓ 1. Endo-H
2. Galactosyltransferase, UDP-Gal
3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 47D

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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$$j\text{-m (independently selected)} = 0 \text{ or } 1.$$
$$n, v-y=0; z=0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

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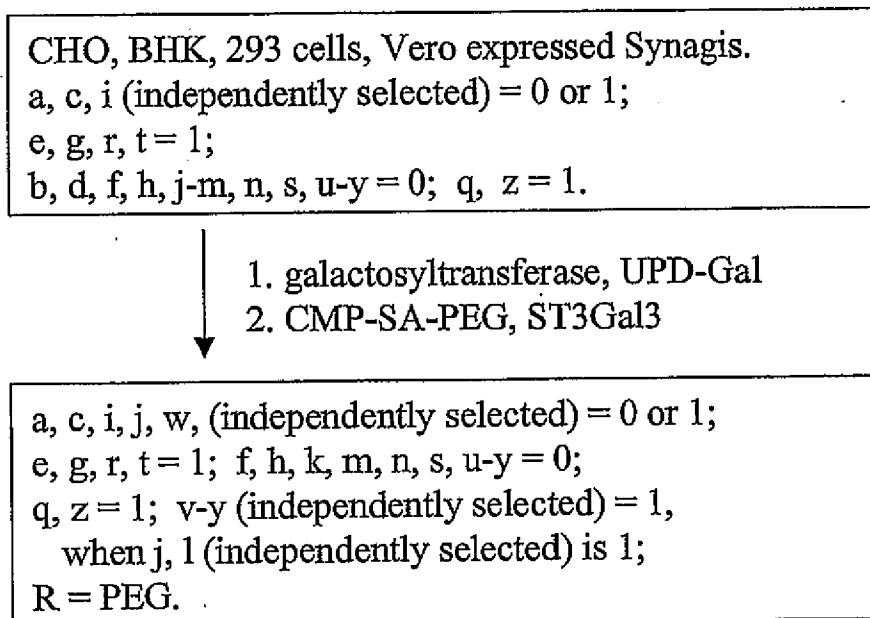


FIG. 48B

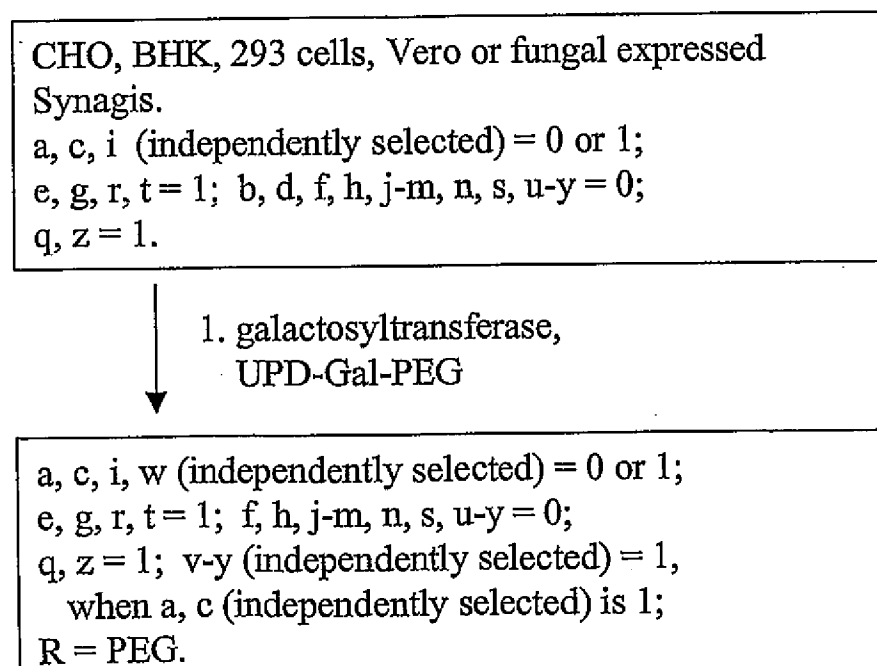


FIG. 48C

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Fungi expressed Synagis.

e, g, i, r, t (independently selected) = 0 or 1;

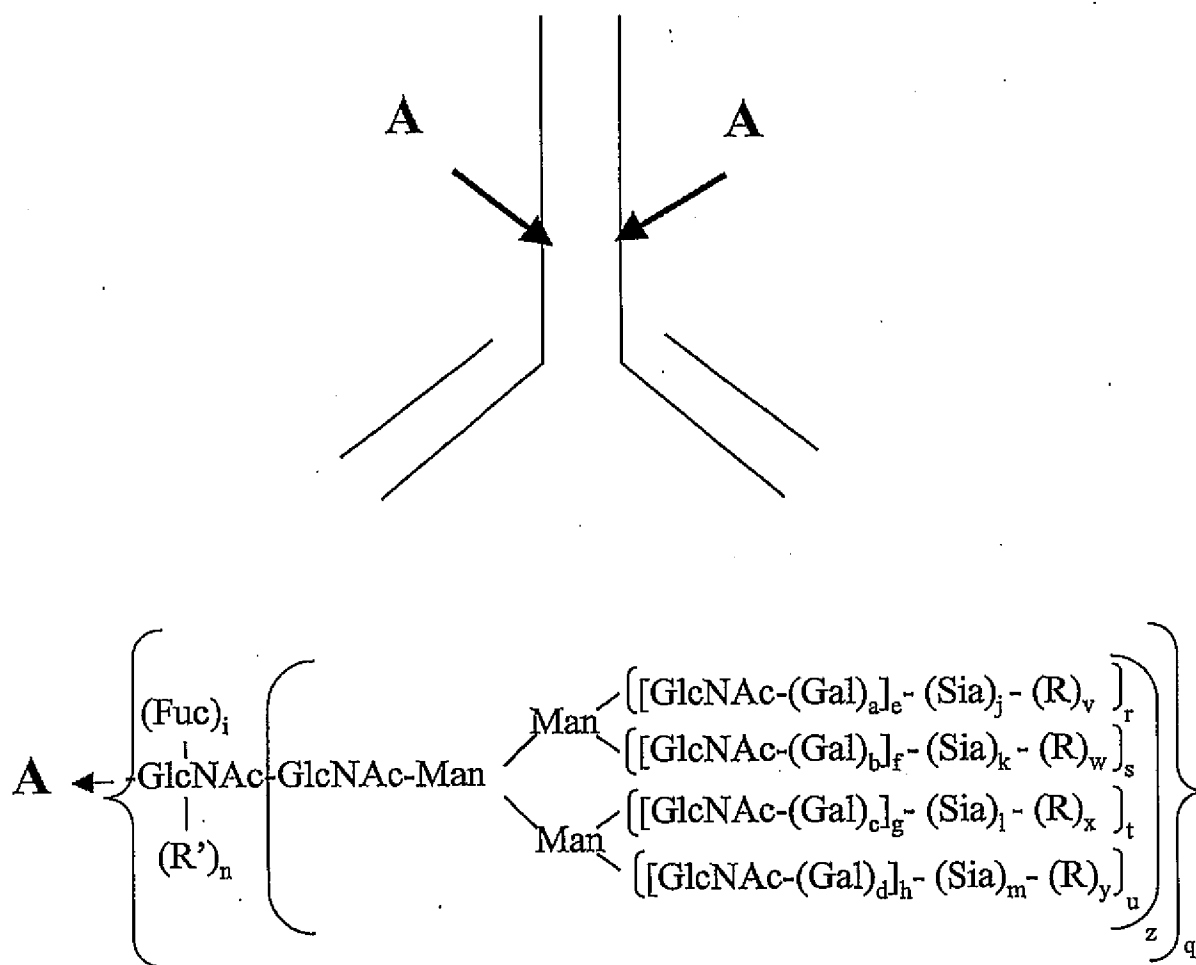
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 48D

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a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

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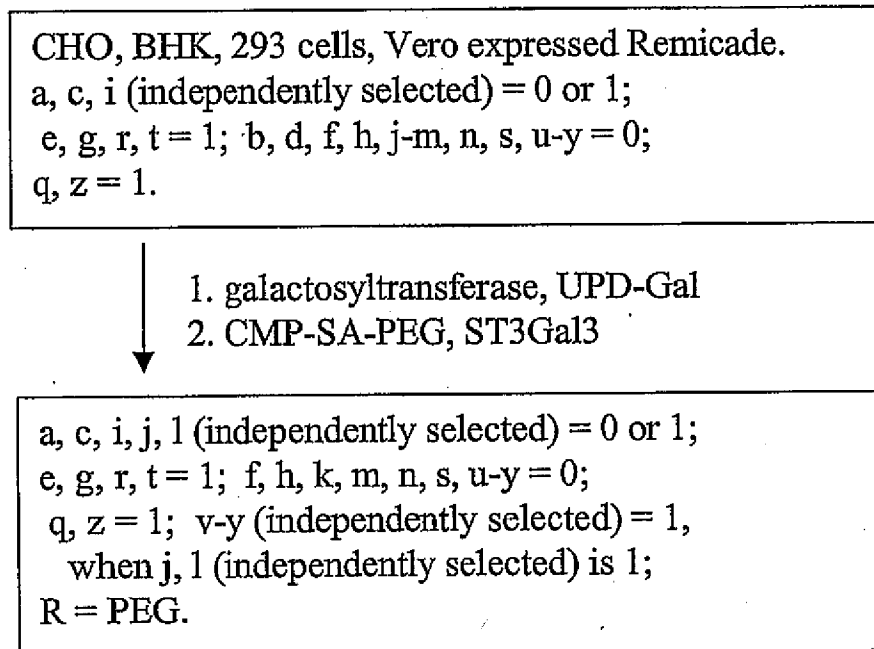


FIG. 49B

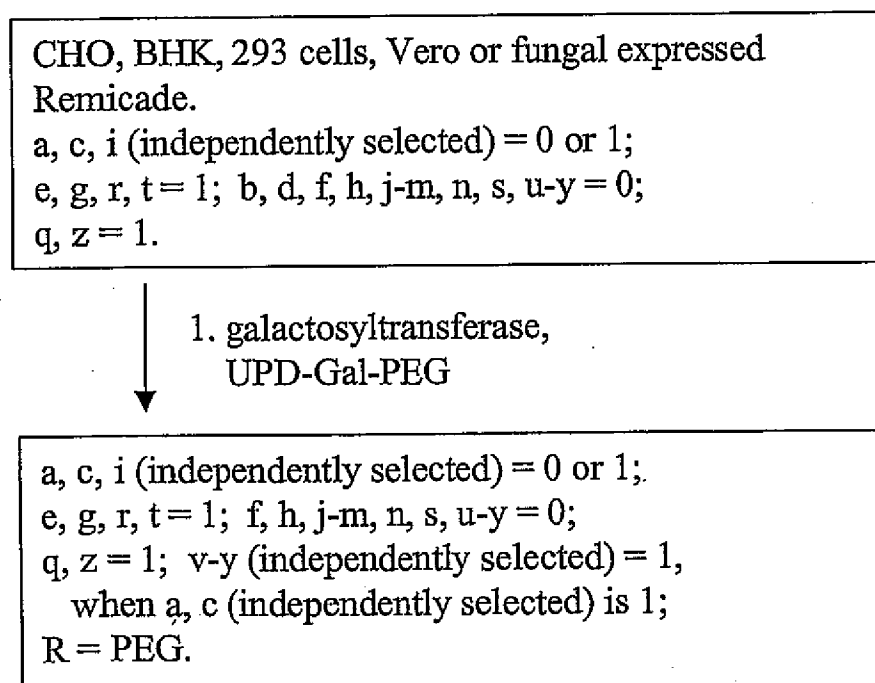


FIG. 49C

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Fungi expressed Remicade.

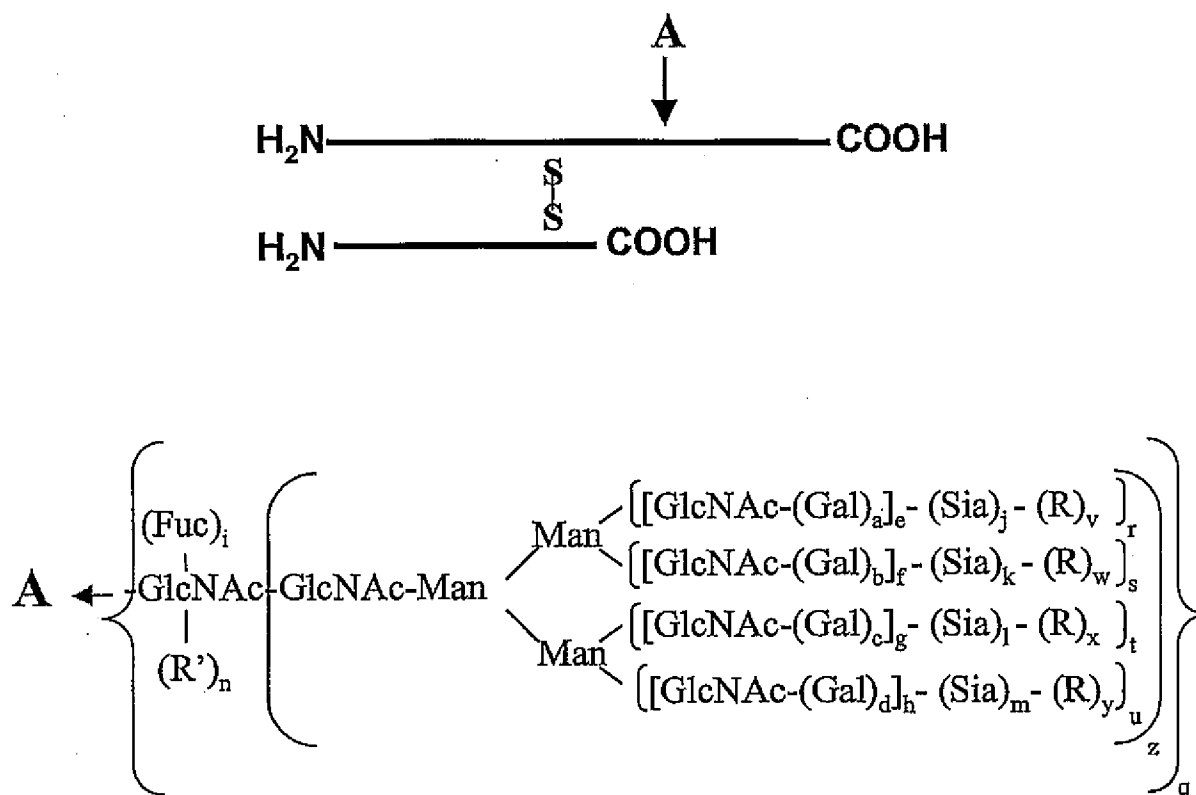
e, g, i, r, t (independently selected) = 0 or 1;
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;
R' = -Gal-Sia-radioisotope complex.

FIG. 49D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 50A

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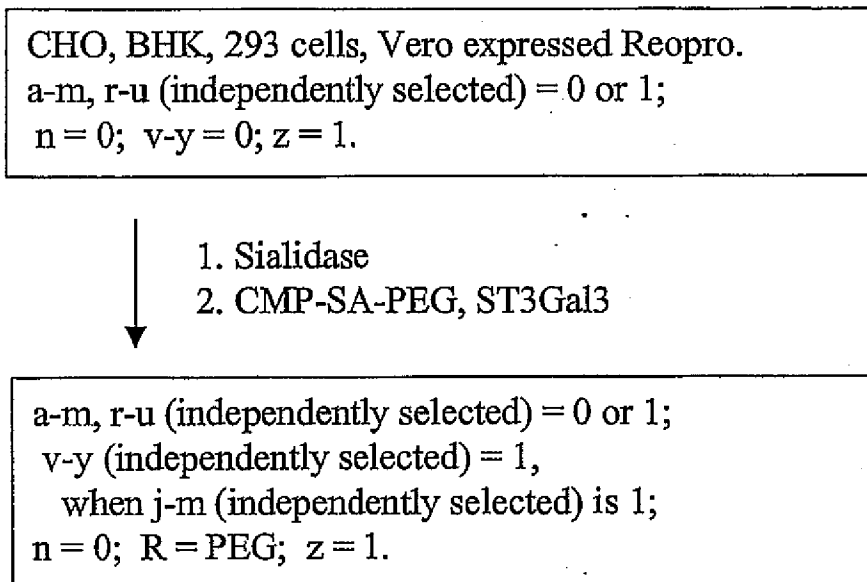


FIG. 50B

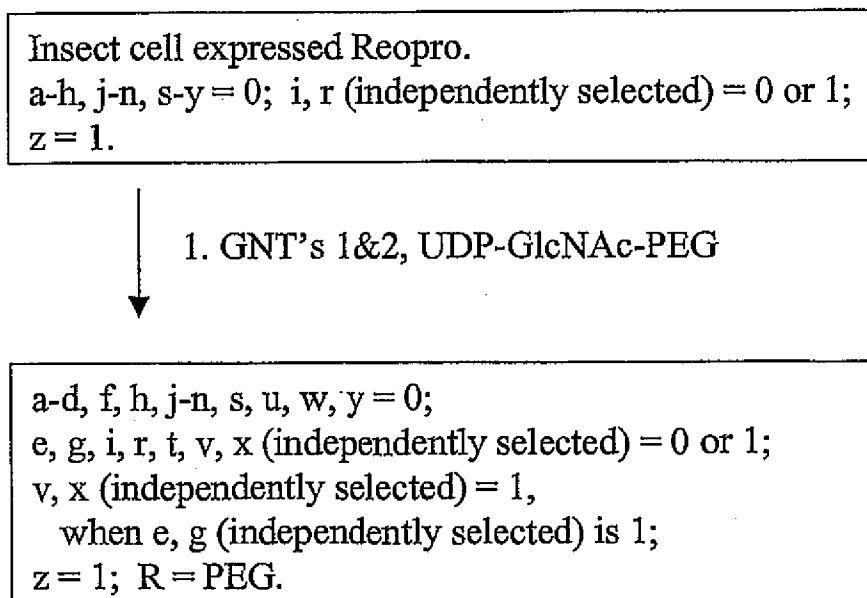


FIG. 50C

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Yeast expressed Reopro.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

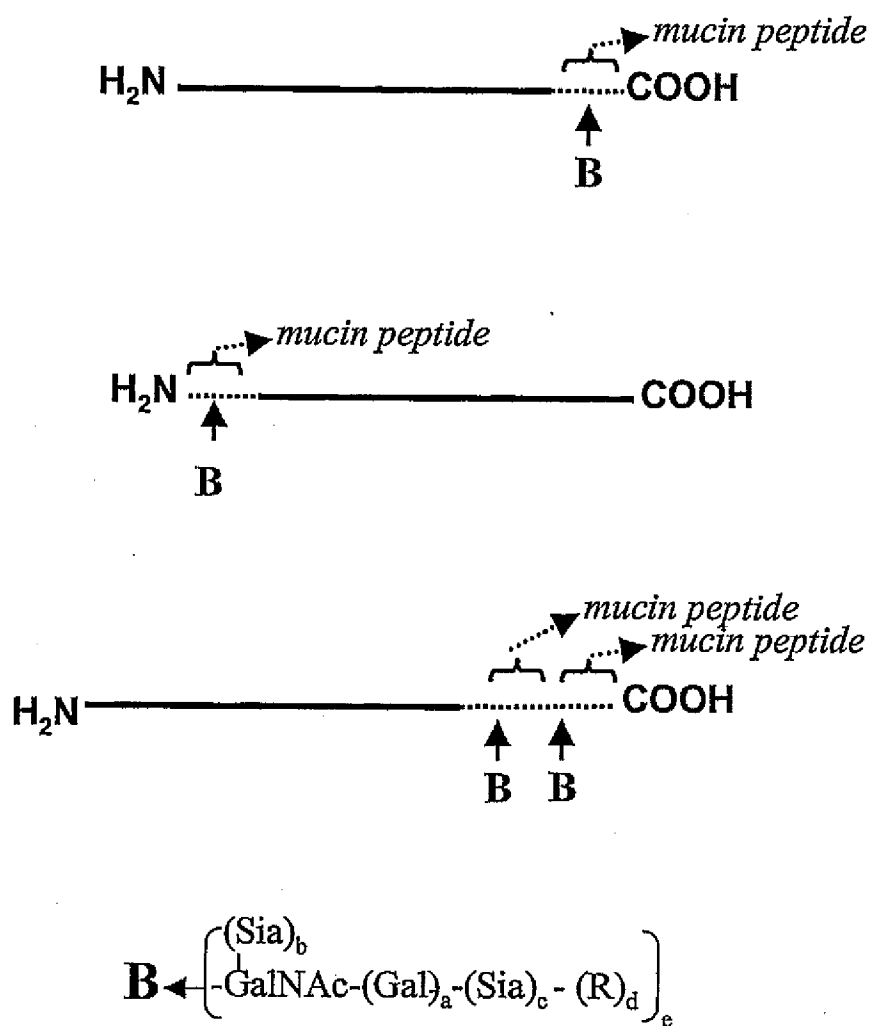
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 50D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 50E

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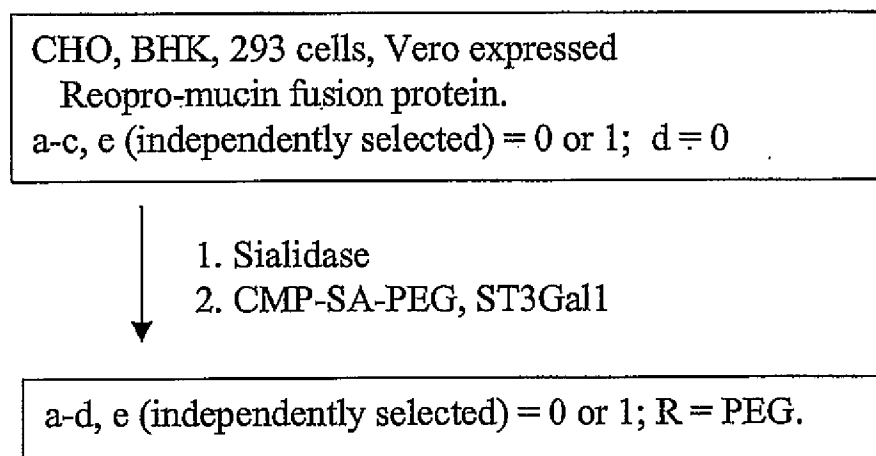


FIG. 50F

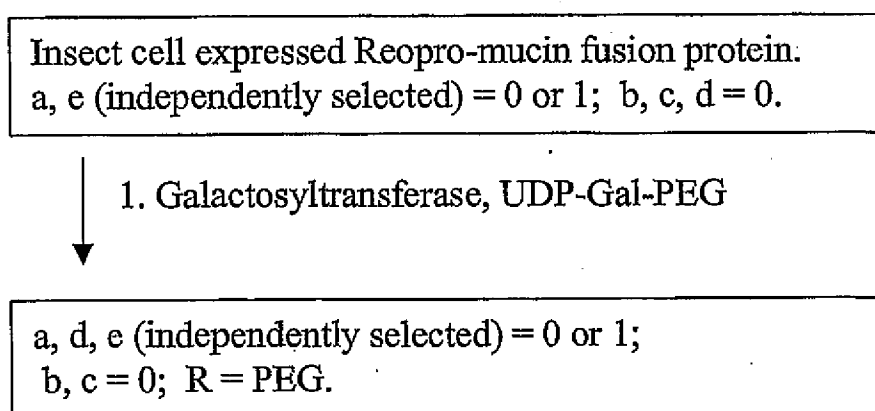


FIG. 50G

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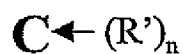
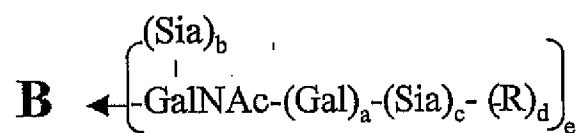
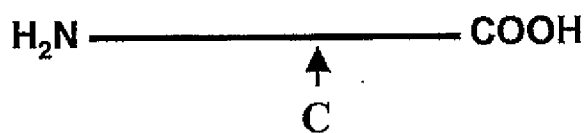
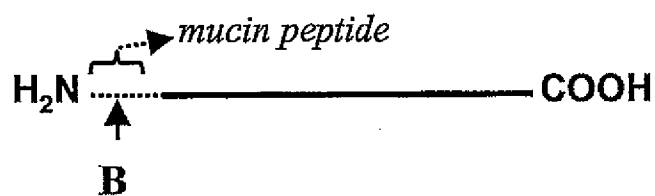
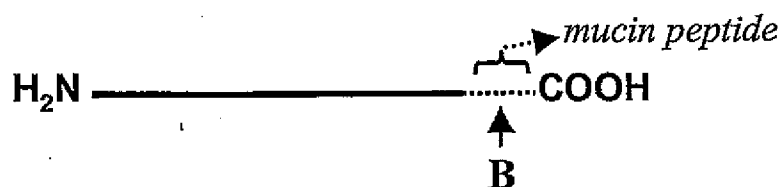
E. coli expressed Reopro-mucin fusion protein.
a-e = 0.

- ↓
1. GalNAc Transferase, UDP-GalNAc
 2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;
a, b = 0; R = PEG.

FIG. 50H

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 50I

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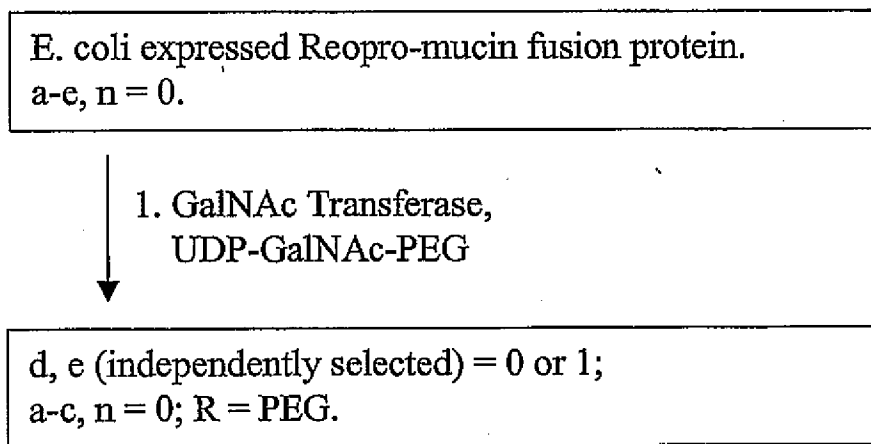


FIG. 50J

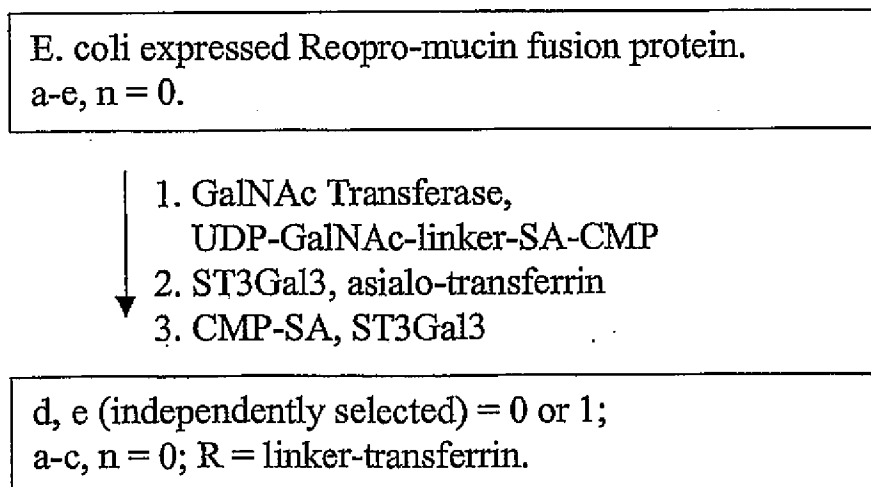


FIG. 50K

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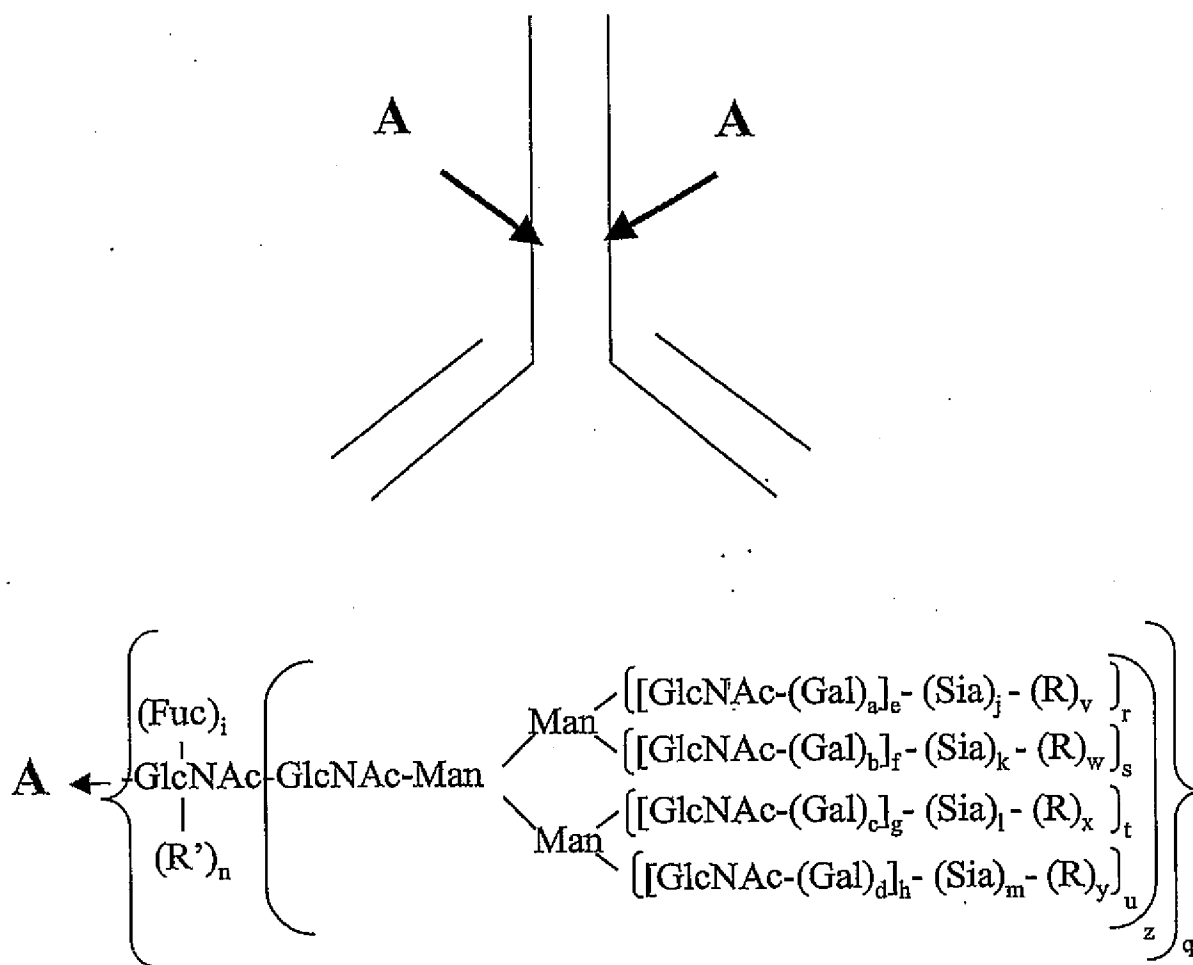
E. coli expressed Reopro(N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 50L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

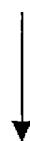
z

FIG. 51A

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1;
f, h, k, m, n, s, u-y = 0; q, z = 1;
v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = toxin.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed
Rituxan.

a, c, e, g, i, r, t (independently selected) = 0 or 1;
b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase,
UPD-Gal-drug

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0; q, z = 1;
v-y (independently selected) = 1,
when a, c (independently selected) is 1;
R = toxin.

FIG. 51C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

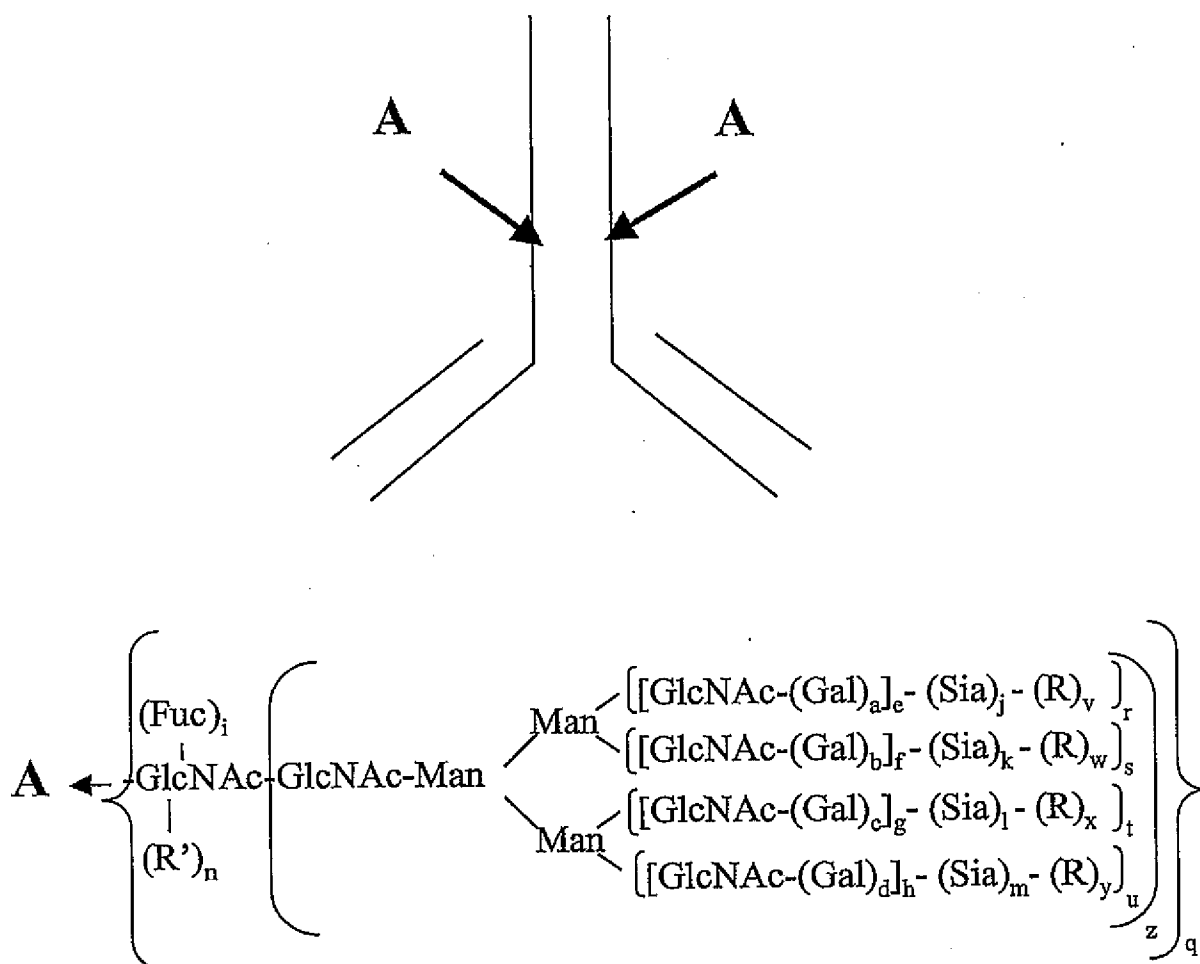
↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$$j\text{-m (independently selected)} = 0 \text{ or } 1.$$
$$n, v-y=0; z=0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51E

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CHO, BHK, 293 cells, Vero or transgenic animal expressed Rituxan.

a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
1. galactosyltransferase, UDP-Gal
 2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when j, l (independently selected) is 1;
 R = PEG.

FIG. 51F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;
 a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;
 R (independently selected) = mannose, oligomannose,
 polymannose.

- ↓
1. mannosidases (alpha and beta)
 2. GNT-I,II, UDP-GlcNAc
 3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;
 R' = -Gal-radioisotope complex.

FIG. 51G

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FIG. 52A

ACCCCCCTGGGCCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA
GCGGCCTTTTCCTCTACCAGGGGGCTCCTGCAGGCCCTGGAAGGGATCT
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCCTGGTTGCCTCCCATCTGCAGAG
CTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG
A

FIG. 52B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

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FIG. 53B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
Arg Ser Lys Glu

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FIG. 54A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTTACAAAGA
AGCAGCAATTTTCAGTGTGAGGAGCTCCTGTGGCAATTGAATGGGAG
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG
AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCATTGACC
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC
TGGAGAAAGAAGATTTTACCAGGGGAAAACCTCATGAGCAGTCTGCAC
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC
AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAT
GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT
TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 54B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 55A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCCTGGAGGAGCTGCGGC
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGGCTCCTGCAAGGACCAGCTCCAGTCCCTATATCTGCTTCT
GCCTCCCTGCCTTCGAGGGCCGGAAGTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTGTCACACCCACAGTTGAATATCCA
TGTGGAAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACCAACGACATC
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTGGTG
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCGCTTCTCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAT
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCACATGCCACCCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA
ACCGTGGGCCACTTTGGGGTGTACACCAGGGTCTCCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCCAGGAGTCCTCC
TGCGAGCCCCATTCCC

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FIG. 55B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

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FIG. 56A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA
AACACTGAAAAGACAACCTGAATTTTGGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCTGATGTGGACTATGTAAATCCTACTGA
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAACTGCTGCCCCTGTGTT
GAAACTGGTGTTAAAATTACAGTTGTGCGCAGGTGAACATAATATTGA
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTCGAGCAATT
ATTCCTCACCACAACCTACAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAACCTGGACGAACCCTTAGTGCTAAACAGCTACG
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCCTCA
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTTGAC
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAGTTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA
AAACAAAGCTCACTTAATGAAAGATGGATTTCCAAGGTTAATTCATT
GGAATTGAAAATTAACAG

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FIG. 56B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

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FIG. 57A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAG
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
GGGGGTTTCAAAGTGGAGAAACCACACGGCGTGCCACTGCAGTACTTG
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
GTGAGATAAACTCTCCTTTTTCCTTACCATAACCACTTTGACACGCTTC
AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAAGCTTG
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 57B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

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FIG. 57C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC
AAAATCCAGAAAACATGTACCTTCAAGGAAGTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 57D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 58A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTG GGGGCTGGCCCT
GCACCGCCGAGCTTCCCGGGATGAGGGCCCCCGGTGTGGTCACCCGG
CGCGCCCCAGGTGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCG
CTCCCTCTGGGGCCTCCAGTCCTGGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
CCTTCGCAGCCTCACC ACTCTGCTTCGGGCTCTGCGAGCCCAGAAGG
AAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCCGCAA ACTCTTCCGAGTCTACTCCAATTTC
CTCCGGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC
GTCGAGGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTCACAGGGGCCAACTTGAGGGGCCAGAG
CAGGAAGCATTTCAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTTACCTGTTTTTCGCACCTACCATCAGG
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTCACGGGCATGGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCTCTGG
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 58B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

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FIG. 59A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCCCGGCGTCTCCTGAACCTGAGTAGA
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA
ACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 59B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 60A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA
AAACCTTAAGAAATATTTTAATGCAGGTCATTCAGATGTAGCGGATA
ATGGAACTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAAC
TTTTAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAATCATCCAAGTGATGGCTG
AACTGTCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTCTGAAGAGCATCCCAGTAA

FIG. 60B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

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FIG. 61A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGGCCTGA
ATTTCAACCTCACGGAGATTCCGGAGGGCTCAGATCCATGAAGGCTTC
CAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTTGCTCTGGTGAATTACATCTTCTTT
AAAGGCCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTTAAACATCCAGCACTGTAAGAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC
CACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG
CTGACCTCTCCGGGGTCA CAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC
TGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATAC
CAAGTCTCCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

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FIG. 61B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

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FIG. 62A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCGTGGGCATCAGGT
GCCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCCGACCTTTCCT
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGGCACAG
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTTCCAGAAAGTGAAG
GGATTTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTCACCCCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA
GTTGCACAACTTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTCACCGAGCCCTGCAGTTGGCCCAGCGTCCCGTTTCACTCC
TTGCCAGCCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG
AGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT
GCTGGGCTGTTGAGTGGATAACCCCTTCCAGTGCCTGGGCTTCACCCCT
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCCTACCCCTCGCC
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC
CACAGCATCATCACGAACCTCCTGTACCATGTGGTCGGCTGGACCGAC
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA
CTTTGTCGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTAA
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC
TGAGGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCG
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCCTGGAGACAATCTCACCTGGCTACTCCATTACACCT
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG
TACTAAAGAGGGGCACAGCAGGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 62A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT
GCCCAGGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC
CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT
TGGAAGACT

FIG. 62B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly
Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu
Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser
Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 63A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCCGATTCAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAAACGCA
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAATATTGCTGGTGCAACAGTGGCAGGGCACAGTGC
CACTCAGTGCCTGTCAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTTCGTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGGCACGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCAACCAACTGGAACAGCAGCGCGTTG
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAACCACAACACTACTGCAGAAACCCAGATCGAGACTCAA
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATT
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT
TTGCCAAGCACAGGAGGTGCGCCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT
TGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG
CCGGA CTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC
CTTGCTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTCAGACT
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC
CAGGCAAACCTTGCACGACGCCTGCCAGGGCGATTTCGGGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAGCAAATGAGATCC

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FIG. 63B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met

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FIG. 64A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA
TGTACAGGATGCAACTCCTGTCTTGCATTGCACTAATTCTTGCCTTG
TCACAAACAGTGACCTACTTCAAGTTCGACAAAGAAAACAAAGAAA
ACACAGCTACAACCTGGAGCATTACTGCTGGATTTACAGATGATTTTG
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC
AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA
GCTCAAAGCAAAAACCTTTCACTTAAGACCCAGGGACTTAATCAGCAA
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTCA
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA
TTAAGTGCTTCCCCTTAAACATATCAGGCCTTCTATTTATTTATTTA
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
TAACTATTATTCTTAATCTTAAACATAAATATGGATCTTTTATGAT
TCTTTTTGTAAAGCCCTAGGGGCTCTAAATGGTTTACCTTATTTATCC
CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG
ATTGGTTAGTAAACCTATTTAATAAATTTGATAAATATAAAAAAAAAA
AAACAAAAAAAAAAAA

FIG. 64B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
Gln Ser Ile Ile Ser Thr Leu Thr

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FIG. 65A-1

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCT
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT
GTACAAAAAGACTCTGTTTGTAGAATTACGGATCACCTTTTCAACAT
CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCC
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT
TCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG
AAGATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG
CCTCATTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTTGCTGTATTTG
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA
GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCAT
CGCCAGGCGTCCTTGGAATCTCGCCAATAACTTTCCTTACTGCTCAA
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTTGTCATATCTCTT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG
ATGATGACAACTCTCCTTCCTTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGAAGTTATAAA
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTTATGGCATAACACAGATGAAACCTTTAAGACTCGTG
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATATTTAAGAATCAAGCAAGCAGA
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT
TCAAGGAGATTACCAAAGGTGTAAACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGATA
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCAATCCA
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGCATCAATGGCTATGTTTTTGATAGTTTGCAGTTGTCAGTTTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA
CTGACTTCCTTTCTGTCTTCTCTCTGGATATACCTTCAAACACAAAAT

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FIG. 65A-2

GGTCTATGAAGACACACTCACCCATTCCCATTCCTCAGGAGAACTGT
CTTCATGTGCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT
AGTTGTGACAAGAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAATGACATAGAGAAGACTGACCCTTG
GTTTGCACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGACAACCTG
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAGTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATTCAA
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAACTACTTCATCAA
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA
GATGCACAAAATCCAGATATGTGCTTCTTTAAGATGCTATTCTTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG
AAAAATCTGTGGAAGGTCAGAATTTCTTGTCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGGTTTTTCCAAGCAGCAGAAACCTATTTCTTACTAACTTGGATAATT
TACATGAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC
TACTGAGCACTAGGCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAATTGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAATTTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCCTA

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FIG. 65A-3

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA
TATATCTGACCAGGGTCCTATTCCAAGACAACCTCTTCTCATCTTCCAG
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAAATAACCTTTCTTTAGCCATTCTAACC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC
GAAACCAGACTTGCCCAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAGTGGAATGAAGCAAACAGACCTGGAAAAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAATCCCAAGAGAAGTCACCAGAAAAAACAGCT
TTTAAGAAAAAGGATAACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCACCAAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAATC
AGAGCCCCCGCAGCTTTCAAAAGAAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAACTAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACCTTTCAGAAATCAGGCCTCTC
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAAGCTTTGTCAAGCCTAATGAAACCA
AACTTACTTTTGGAAGGTGCAACATCATATGGCACCCACTAAAGAT
GAGTTTGACTGCAAAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTCACCATCTTTGATGAGACCAAAGCTGGTACTTCACT
GAAAATATGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAACATCCATTCT
ATTCATTTCAAGTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA
TAAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGGA

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FIG. 65A-4

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTCAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAAGGAG
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG
TGGATTCATCTGGGATAAAACACAATATTTTAAACCCTCCAATTATTG
CTCGATACATCCGTTTGCACCCAACTCATTATAGCATTTCGCAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACTACTCAGGGAGTAAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGA
CTCCTTCACACCTGTGGTGAACCTCTCTAGACCCACCGTTACTGACTCG
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCCTCAGCTCCAGG
GCAGTGTCCCTCCCTGGCTTGCCCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAGCCTCCTGAATTAATCATCAGTCCTGCATT
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTAACTTAACTCTTA
CCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACT
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTTCTCCCTG
AAAAGTTAGGCCTCTCAGAGTCACCACTTCCTCTGTTGTAGAAAACT
ATGTGATGAACTTTGAAAAAGATATTTATGATGTTAACATTTTCAGGT
TAAGCCTCATACGTTTAAAATAAAACTCTCAGTTGTTTATTATCCTGA
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAAGGCAAATCATTTGGACAATCTGCAAAATGGAGAGAA
TACAATACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGA
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA
AACTAGCATTCTTAAACTGAGAATTATAGATGGGGTTCAAGAATCCC
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA
AAATGATGA

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FIG. 65B-1

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe
Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp

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FIG. 65B-2

Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro
Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu

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FIG. 65B-3

Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
 Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile
 Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
 His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
 Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
 Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
 His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
 Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
 Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
 Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
 Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
 Leu Thr Arg Tyr Leu Arg Ile His

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FIG.65B-4

Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu
Ala Gln Asp Leu Tyr

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FIG. 66A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAATTCGGAGGGGCAGCACTGTGAAATAGATAAGTCAAAAAC
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCGCGCCCTGCCTGCCCTGGAACCTCTGCCACTGTCCTTC
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCCTGG
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCTGG
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTCCAAGAGTGCATGGT
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCCCGCTTTAAGATTA
TTGGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTTCGGGCC
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTTCGCTCAA
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAC
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCCACCGGGAGTGTCAGCAGCCCCACTACTACGGCTCTG
AAGTCACCACCAAAATGCTGTGTGCTGCTGACCCACAGTGGAACA
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCCAGGGAGGAAACGGGCACCAACCCGCTTTCTTGCTGGTTGTC
ATTTTTGCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

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FIG. 66B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

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FIG.67A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTTCGTGTA
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGGTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGCCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTT
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAACTGCAG

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FIG. 67B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

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FIG. 68A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACC CGCCGCTCCTGCACCGAGAGAGA
TGGAATAAAGCCCTTGAACCAGC

FIG. 68B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 69A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTCACCCCACCACACGGCGGTCTTTTGGGGTGGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG
TTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAACCTCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGGCCTATATTTTCCT
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCTGTTCCGACTACTGTC
TACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC
ATGGAGAGCACAACATCAGGATTCCTAGGACCCCTGCTCGTGTTACA
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG
TCCTGGCCAAAATTTCGAGTCCCCAACCTCCAATCACTCACCAACCTC
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT
ATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
GGAAACTGCACTTGTATTCCCATCCCATCATCCTGGGCTTTCGCAAGA
TTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTTGTTCAAGTGGTTCGCAGGGCTTTCCCCCACTGTTTGGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC
ATTGA

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FIG. 69B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

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FIG. 70A

CGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGC
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
AAGTATTCATTCCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG
GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
GAAGGACATGGCAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCG
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT
GCCACCAAGCCTTGTCCTAATAAAATTAAGTTGCATC

FIG. 70B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 71A

ATGGCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCGCCCAGGTGGCATTACACCCTA
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATAACCCAGCTCTGGAAGTGGGTTCCCGAGTGCTTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC
ACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGCTCC
AAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGC GTTGGACAGAAGGGCGCCCACTCGGAACCAGC
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG
TCAATGTCACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGCTGCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCTTCTCCAAGGA
GGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG
GGAGCACCGAAGAGAAGCCCCTGCCCCCTTGGAGTGCCTGATGCTGGG
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTGCTAGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGGCCCTGGTCCTT
CCAGGC

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FIG. 71B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

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FIG. 72A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 72B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

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FIG. 73A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 73B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 74A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC
ATCCACTGGTATCAGCAAAGAACAAATGGTTCTCCAAGGCTTCTCATA
AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC
AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
ACGTTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG
TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
AGGTTCACCATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
ATGACCGACTTAAGAAGTGAAGACACTGGCGTTTATTACTGTTCCAGG
AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
ACAGTCTCC

FIG. 74B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 75A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTC
CA GGTTCCTACTGGTGACGTCAGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGCCGGCGAGGCGGCGGTTCGACA
AAACTCACACATGCCACCGTGCCAGCACCTGAACCTCCTGGGGGGA
CCGTCAGTCTTCCTCTTCCCCC AAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACG
CCTCCCGTGTTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGGAAATGA

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FIG. 75B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 76

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 77

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
Leu Val Thr Val Ser Ala

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FIG. 78

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

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FIG. 79

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser

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FIG. 80

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
Ser Phe Asn Arg Gly Glu Cys

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FIG. 81

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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FIG. 82A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTTCGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTCTGGAGGGGGGACCAAGCTGGAAATC
AAA

FIG. 82B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 83A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT
ACCAGTTACAATATGCACTGGGTAAACAGACACCTGGTCGGGGCCT
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 83B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

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FIG. 84A

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCCAACCGTGCCCAAGCAGCCTGAACTCCTGGGGGGACCGTCAGTCTTC
CTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA
TCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTCAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTTCGTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTGA
CCCTGGAAGGTGCCACTCCCCTGTCCTTTCCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA
ATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 84B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGGCACAGCGGCCCTGGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCCAACCGTGCCCAAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTC
CTCTTCCCCCCTAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTCAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTGA
CCCTGGAAGGTGCCACTCCCAGTGTCTTTCCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA
ATGAGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 84C

GCTGCGATTTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAAGTGCAT
CGTCGCCGTGTCCCAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTGAGAACAATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCC
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGC
TCCCCTCCTAAAGTCATGCATTTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT
TTGCCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAC
TGTCCTTTCTAATAAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT
ATTTGCATAATGAGAAAAAAGGAAAATTAATTTTAACACCAATTCA
GTAGTTGATTGAGCAAATGCGTTGCCAAAAGGATGCTTTAGAGACA
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGGAGTACCC
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGA
AATATGCTTGTTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTGACGCGAGGGGCGCCCGGTTCTTTTTGTCAAGACCGA
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT
CGTGGCTGGCCACGACGGGCGTTCTTGGCGAGCTGTGCTCGACGTTG
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATC
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAATCG
GATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATC
AGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATG
CCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

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FIG. 84D

AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT
GCTTTACGGTATCGCCGCTTCCCGATTTCGCAGCGCATCGCCTTCTATC
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC
CGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCG
CCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATA
GCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT
GTGGTTTGTCCAAACTCATCAATCTATCTTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGG
AGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCAC
ATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC
GGTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
TGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC
CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG
GCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAAGTC
GTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGAC
CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA
CAAACCAACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATT
ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGG
TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTA
AATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC
GAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGC

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FIG. 84E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGGCGACCGAGTTGCTCTTGCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCA
GCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA
TACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACA
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

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FIG. 85A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGGCGGAACCTGGGCG
GAGTTAGGGGCGGGATGGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATCCCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT
TATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGGCGTGGATACC
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATTGACGTCAATG
GGAGTTTGT TTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTCACTATGGATTTTTCAGGTGCAGATTAT
CAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT
TGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGGAGAA
GGTCACAATGACTTGCAGGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGT
CTGGGACTTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCCG
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCC
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTTGAATTCAGATCCGTAAACGGTTACCAACTA
CCTAGACTGGATTCGTGACAACATGCGGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCCTGTCTTTCC

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FIG. 85B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTCAATG
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTG
ACTCACGGGGATTTCOAAGTCTCCACCCCATTTGACGTCAATGGGAGTT
TGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCT
CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGA
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTTGCTACGCGTGTCTGTCCCAGGTACAACCTGCAGCAGCCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGA
CACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAAT
GGTGATACTTCCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACC
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACAC
ATGCCACCCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC
ATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTG

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FIG. 85C

GACAACATGCGGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG
ACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCAT
AATGAGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGA
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTGCGATTTCCG
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTCGACCATTGAACTGCATCGTCGCCCGTGTCC
CAAAATATGGGGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCT
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTCTTCAG
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC
TCCATTCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT
CTCAGTAGAGAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGC
CAAAAGTTTGGATGATGCCTTAAGACTTATTGAACAACCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTG
GGGAAATATAAACTTCTCCCAGAATACCCAGGCGTCCTCTCTGA
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCTCCTAA
AGCTATGCATTTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCC
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTTATTTGCATAATG
AGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCTGCA
CAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAGACT
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

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FIG. 85D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC
AGCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA
CGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGAACGTTCGCCAGGCTCAAGGCGCGCATGCCCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG
GAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT
CGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA
GTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGAC
GCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGA
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGTT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA
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GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCTCGGCT
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GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC
ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCC
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CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGTTGCTCCAA
GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT
ATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

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FIG. 53A

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ACTTTTAAATTTAATGTATAGAATAGAGATATACATAGGATATGTAAA
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CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCCTCCAGGAGGAGTTTGG
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GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG
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GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
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CTTCATTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA
AACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT
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FIG. 85E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
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TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC
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TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
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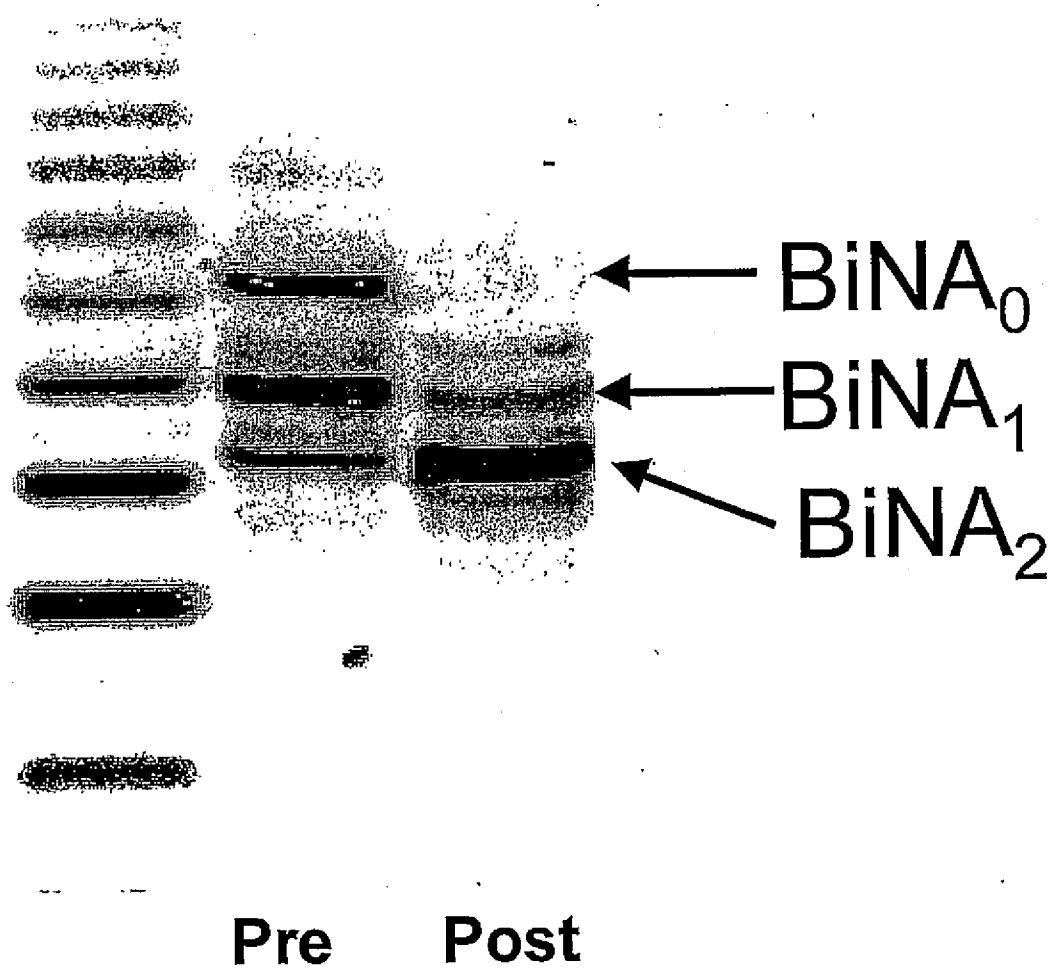


FIG. 86

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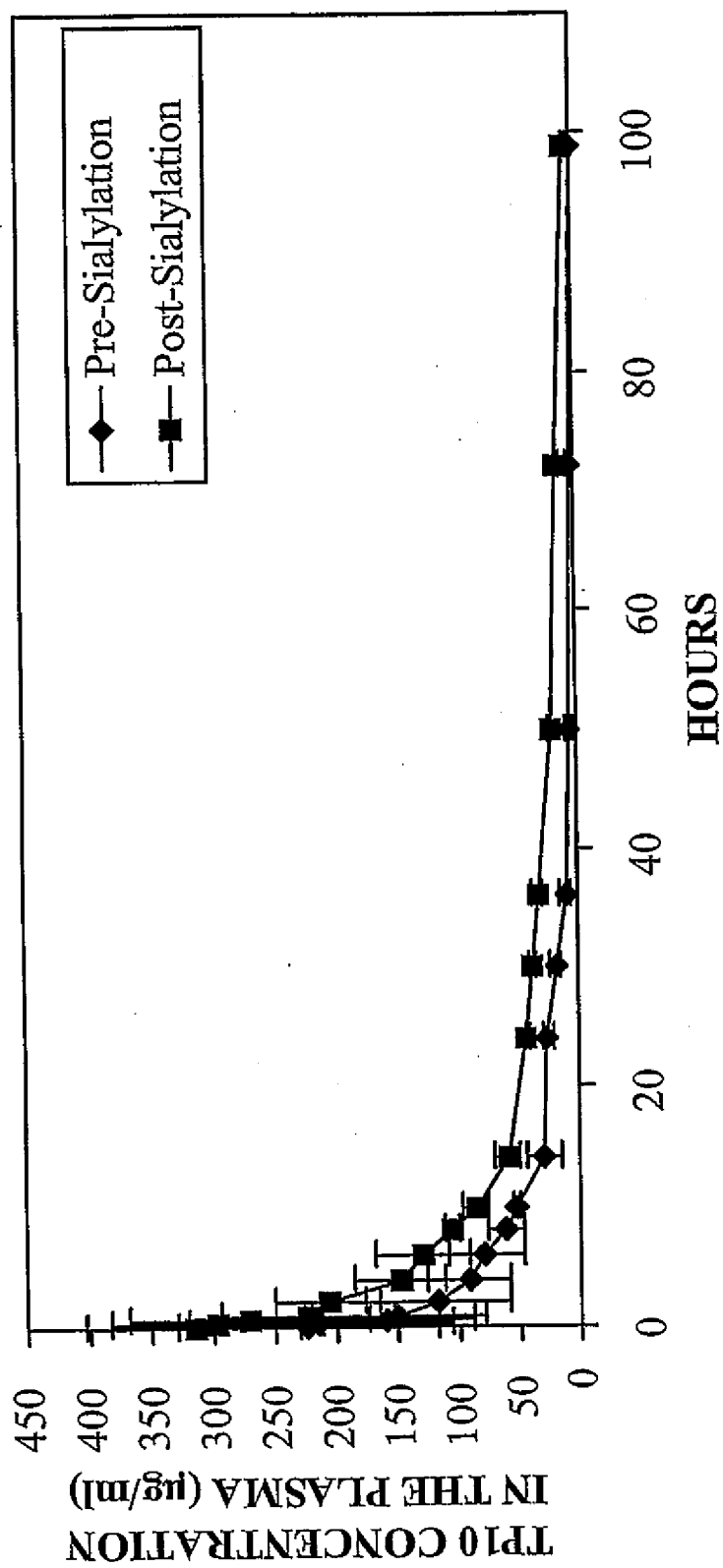


FIG. 87

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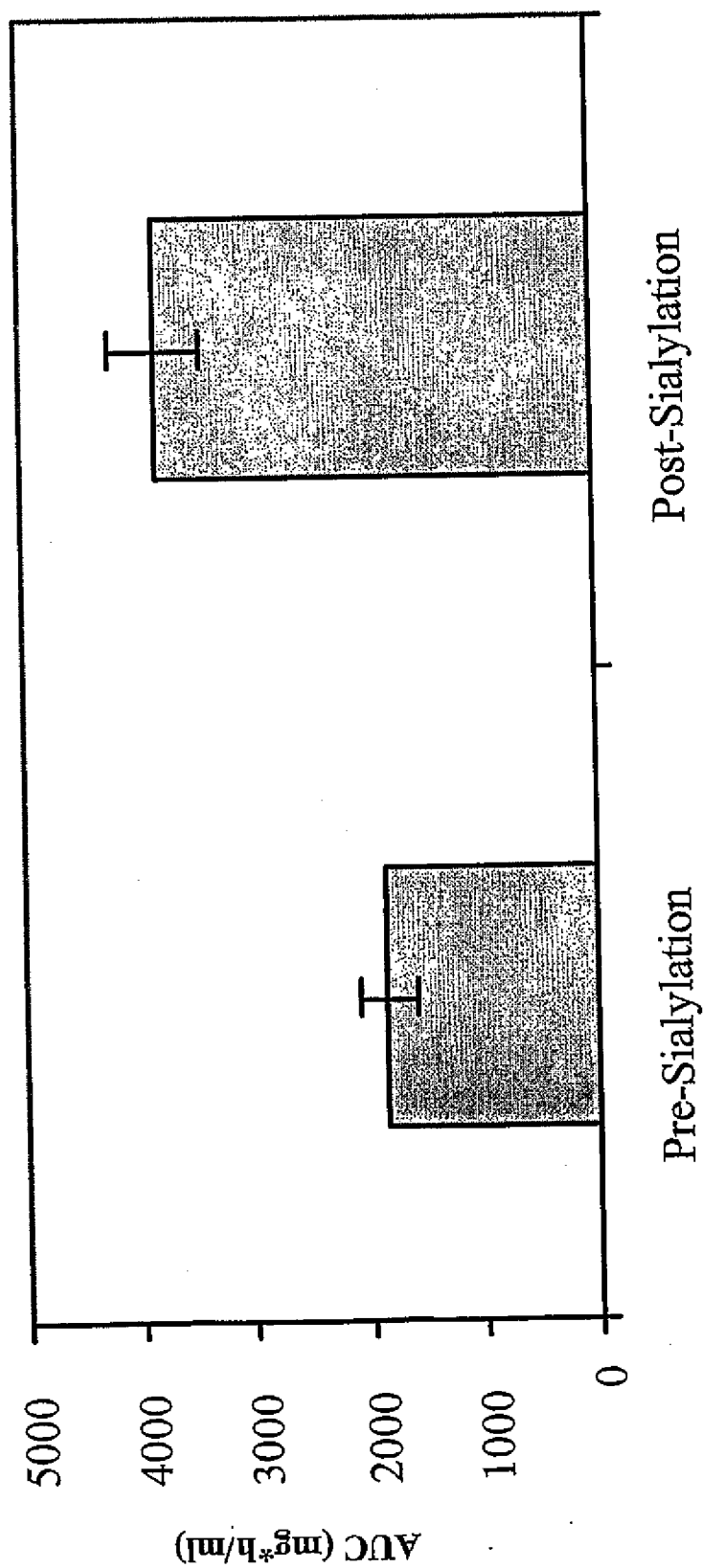


FIG. 88

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← BiNA₂F₂

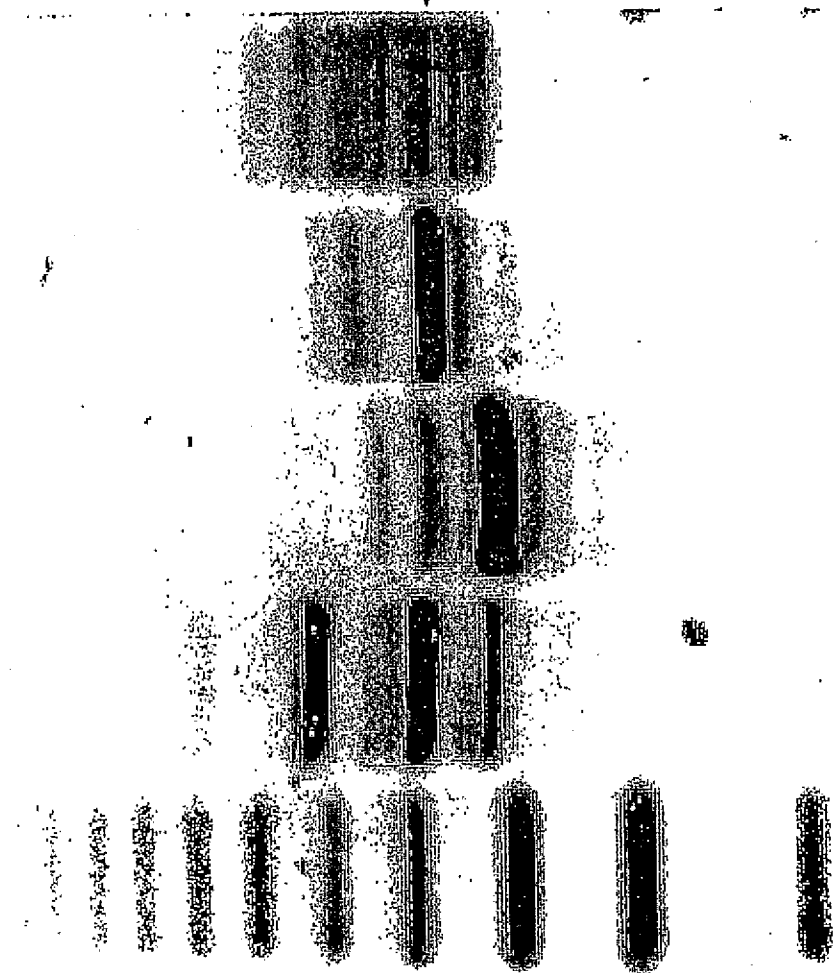
FIG. 89

TP20

+F

+SA

Pre



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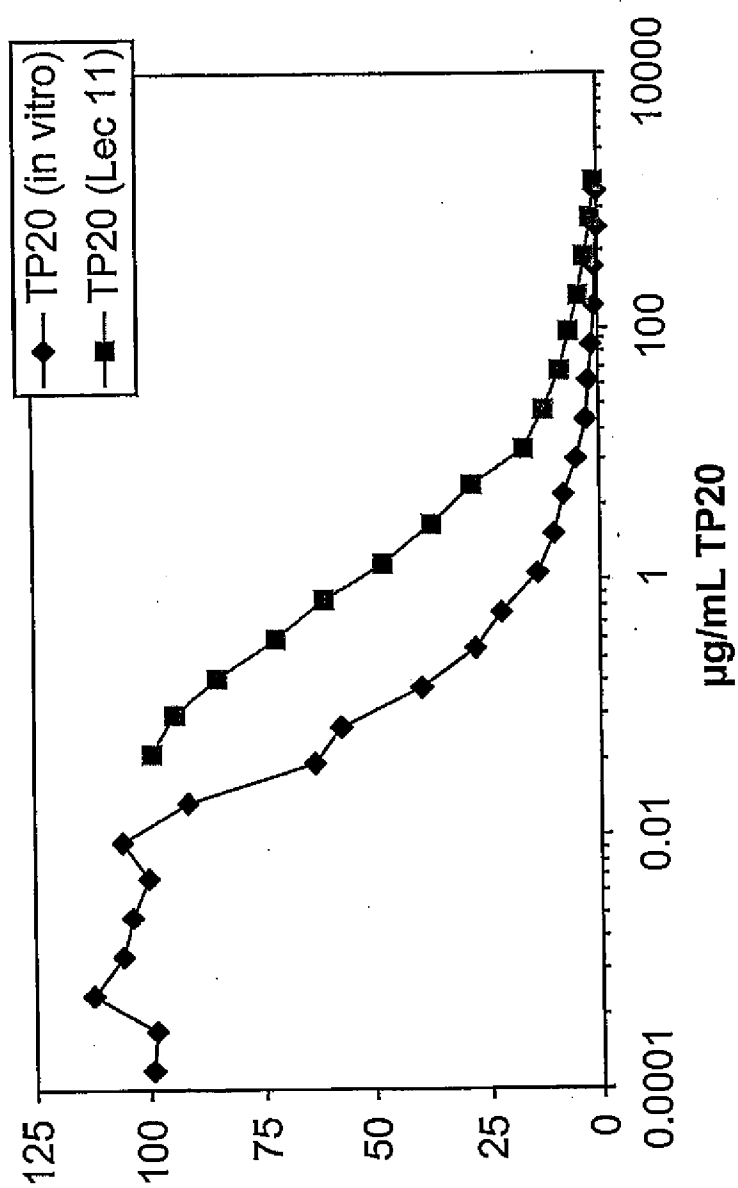


FIG. 90

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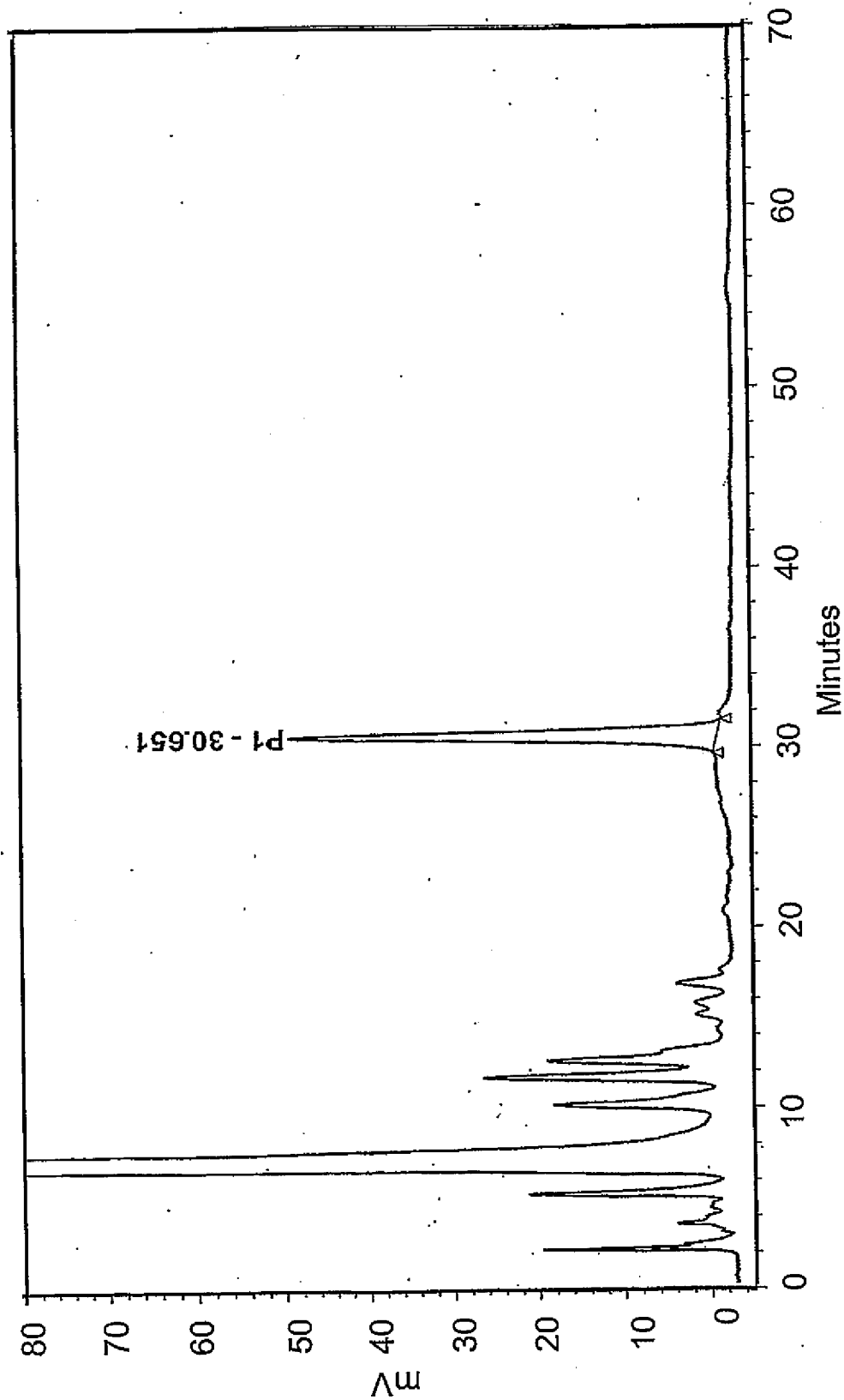


FIG. 91

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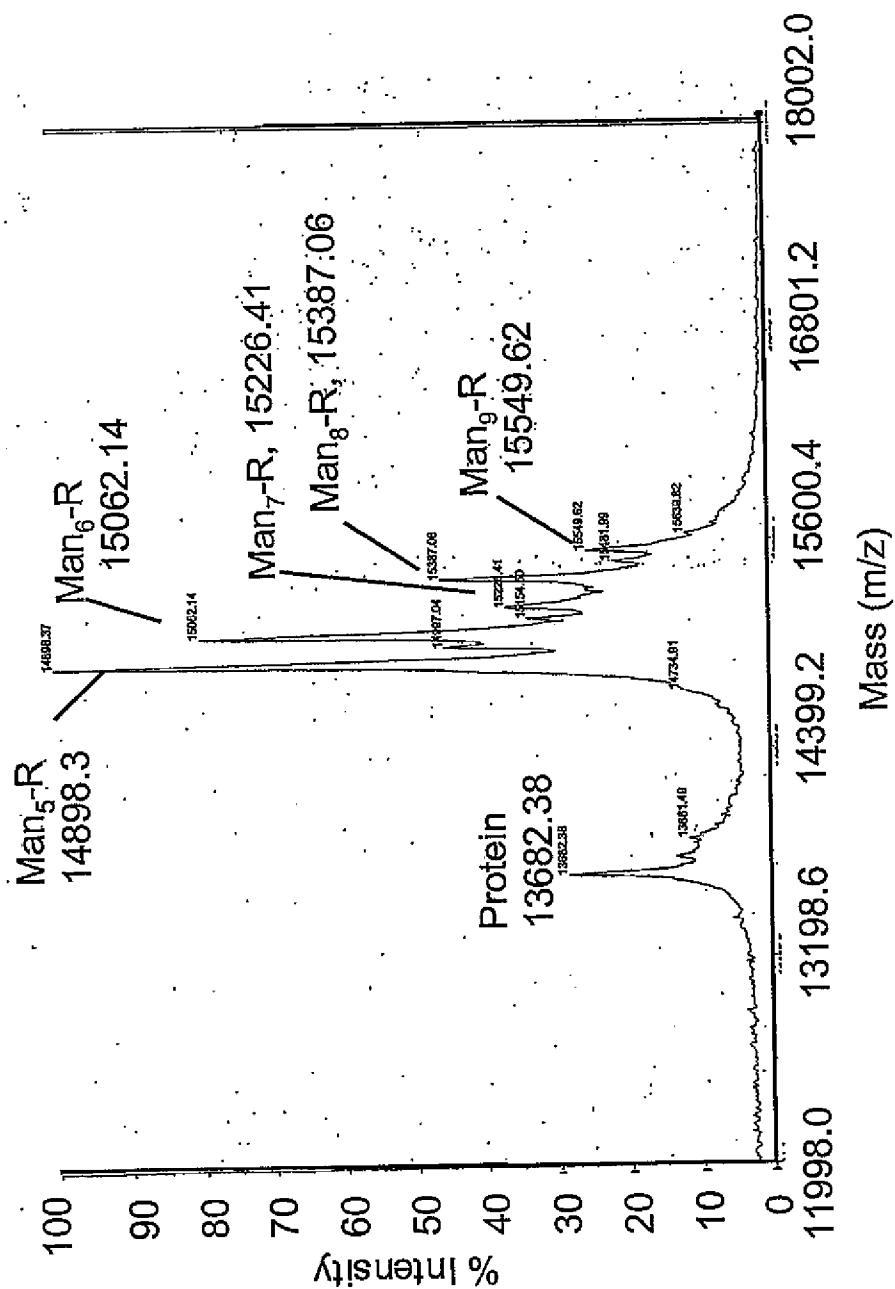


FIG. 92A

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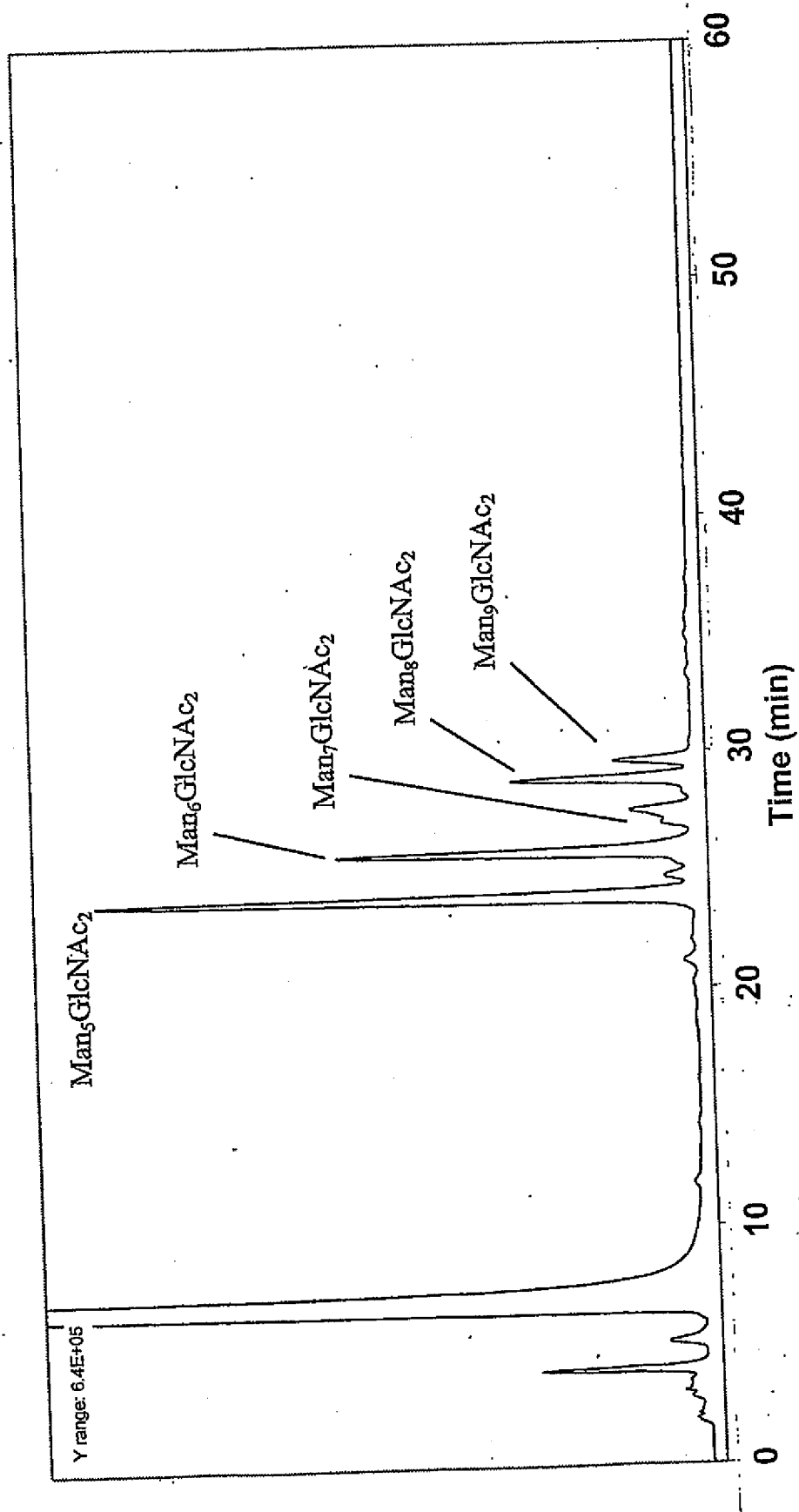


FIG. 92B

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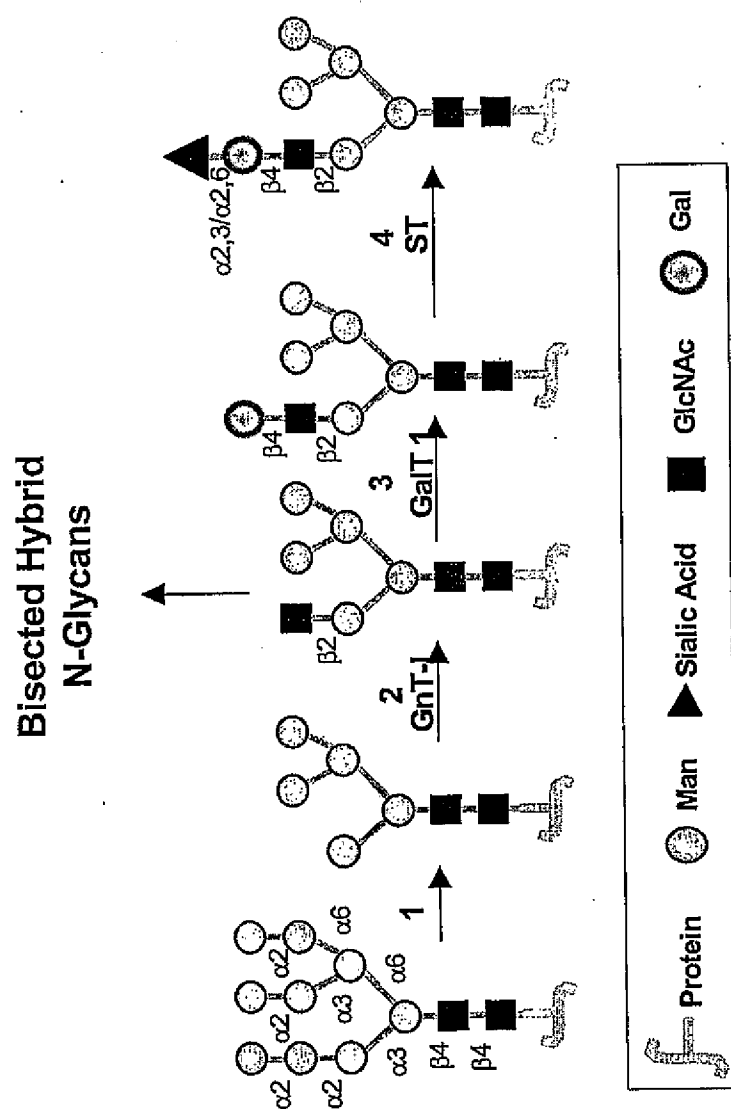
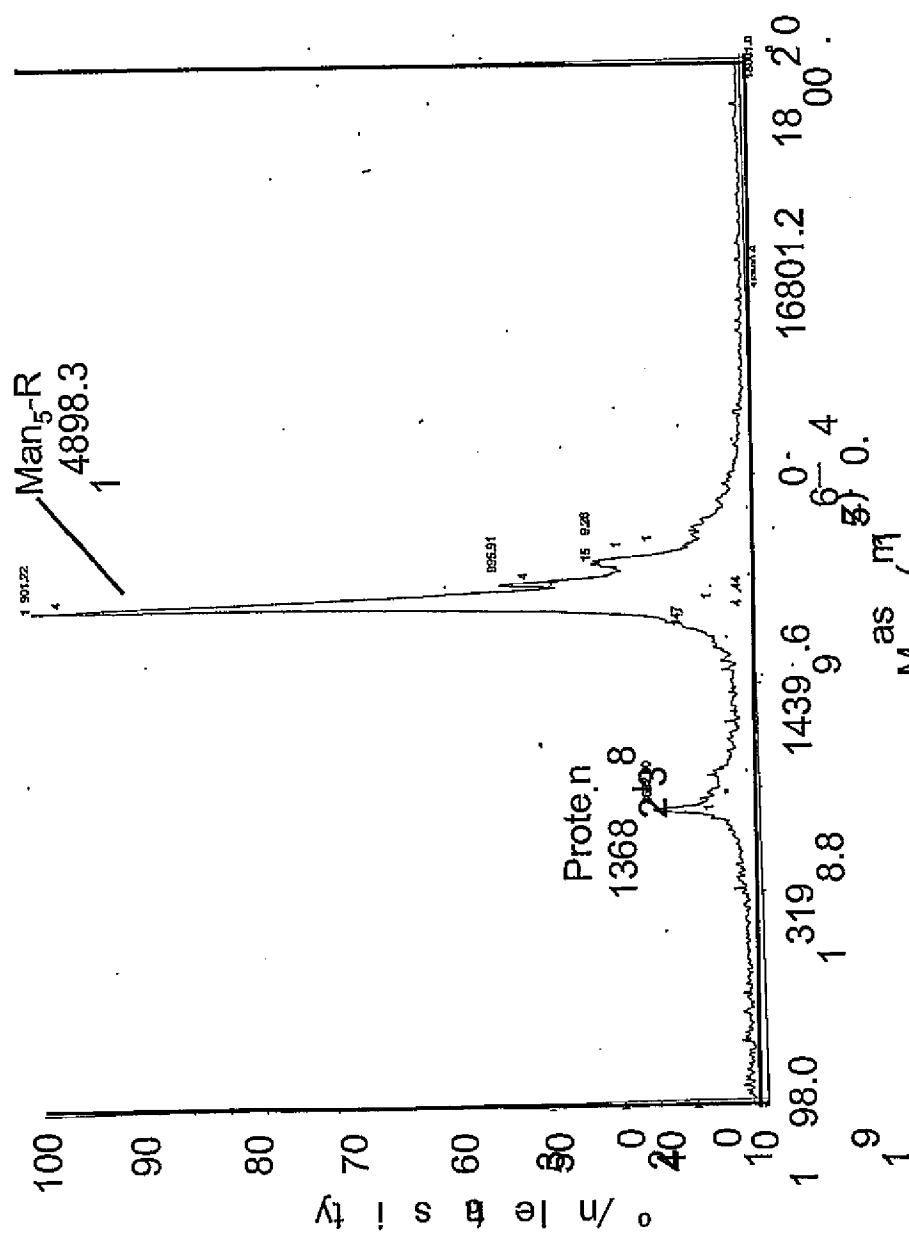


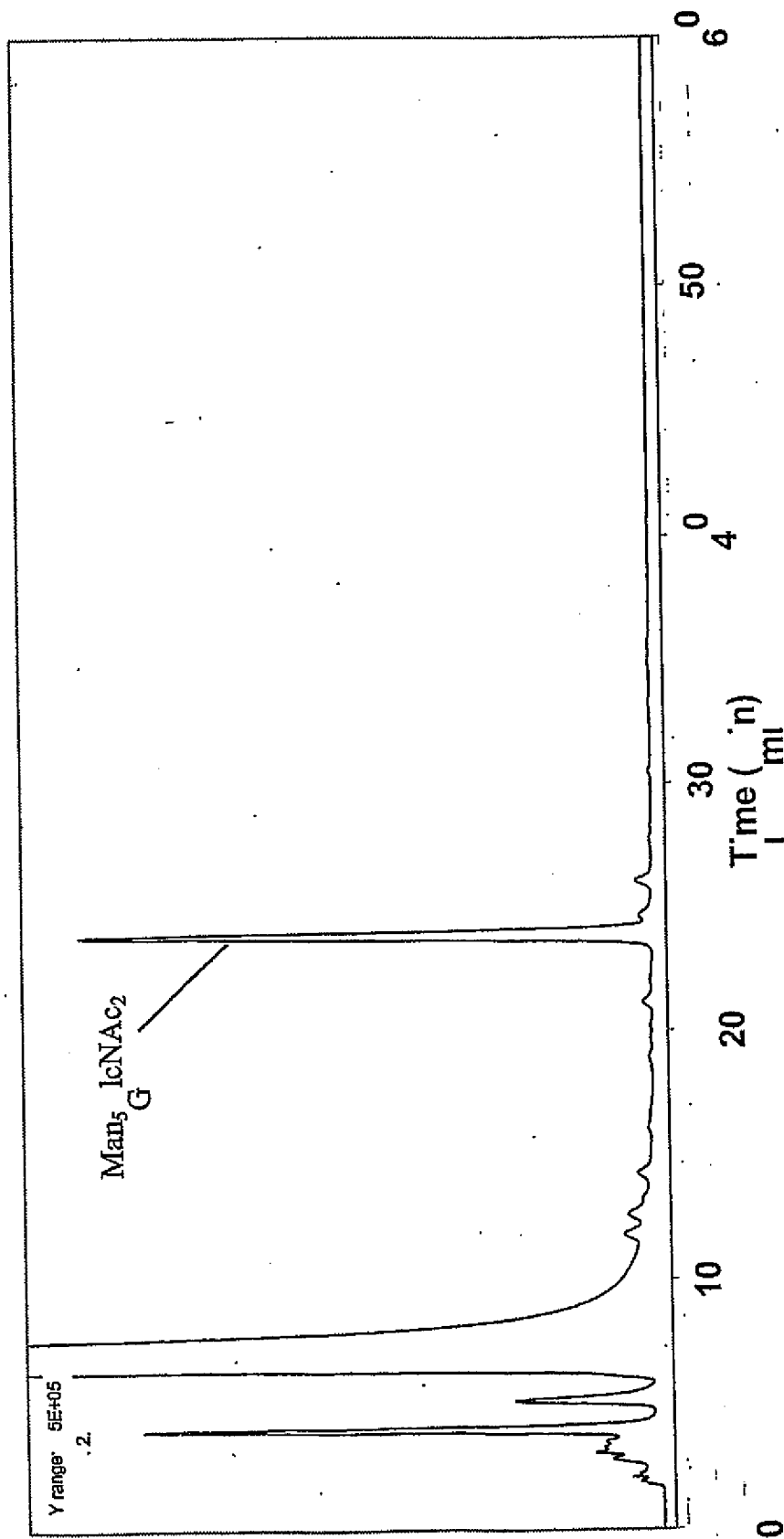
FIG. 93

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FI 94A

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F 94B
IG

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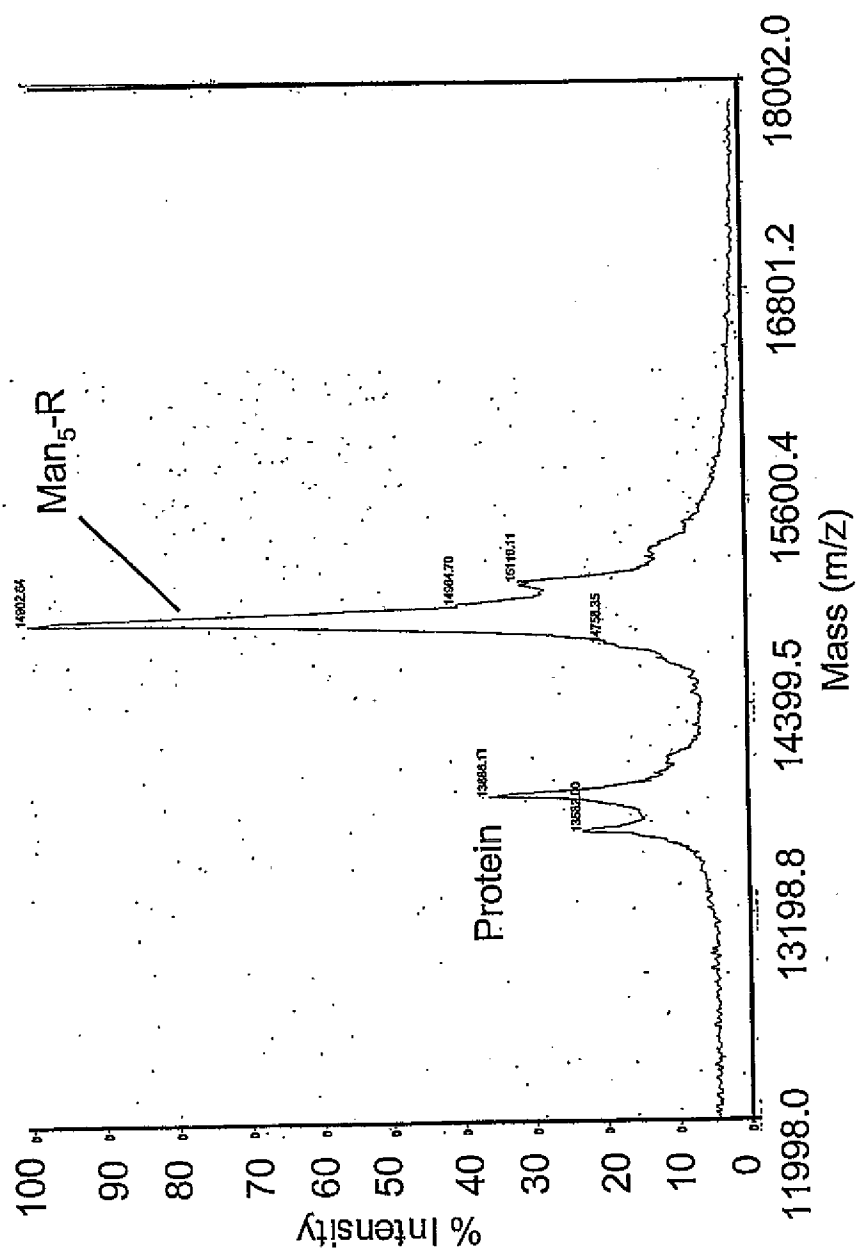


FIG. 95

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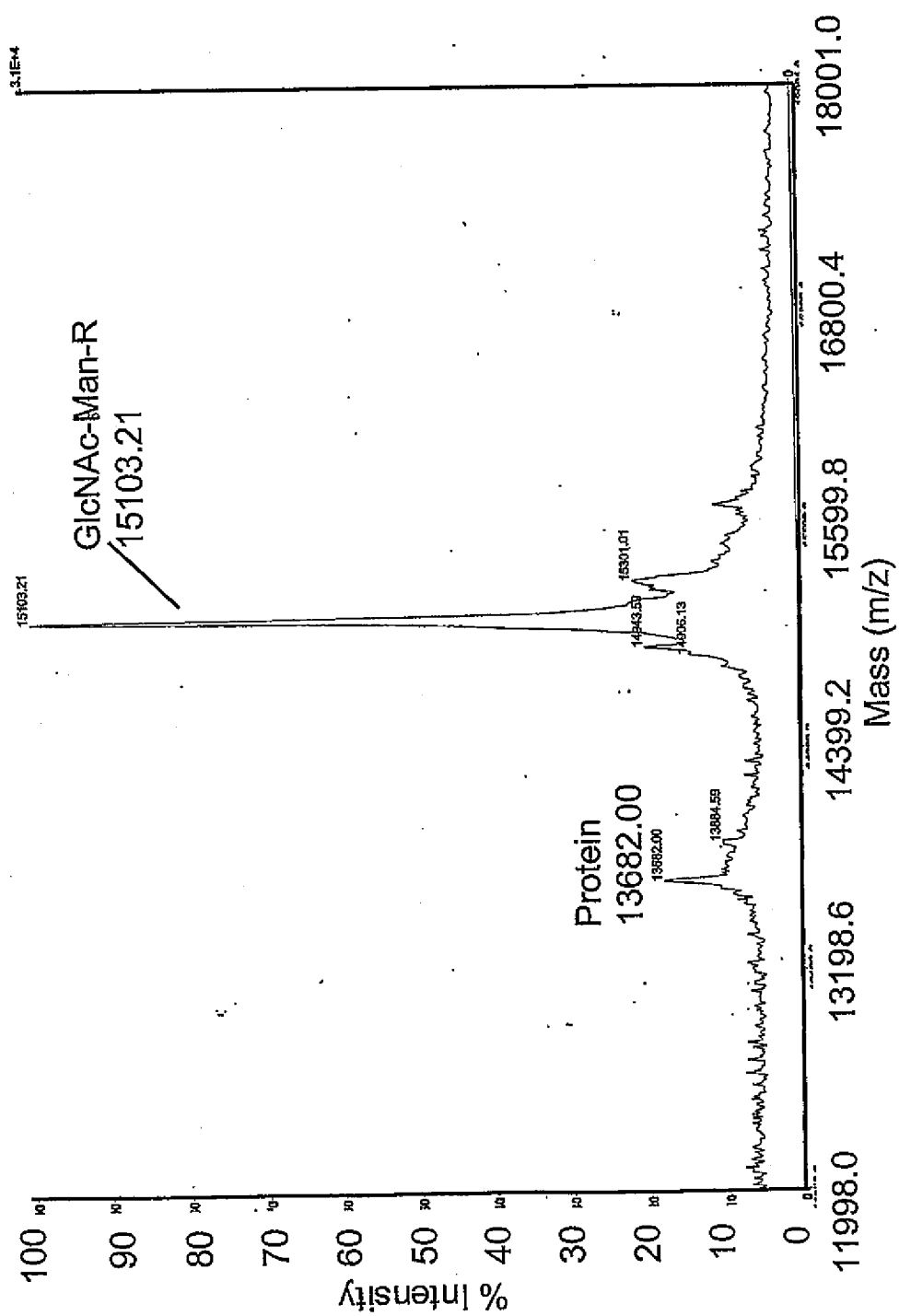


FIG. 96

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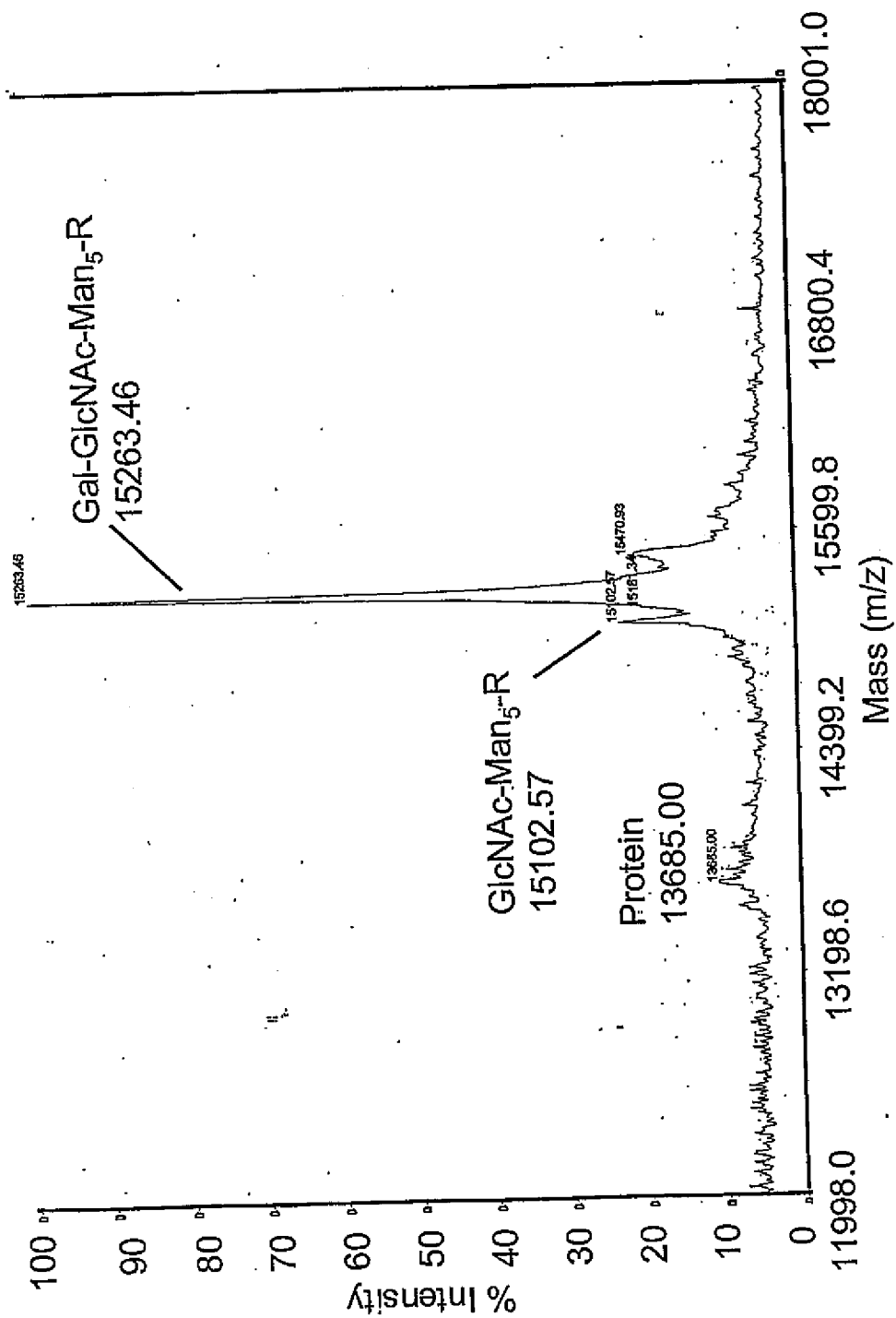


FIG. 97

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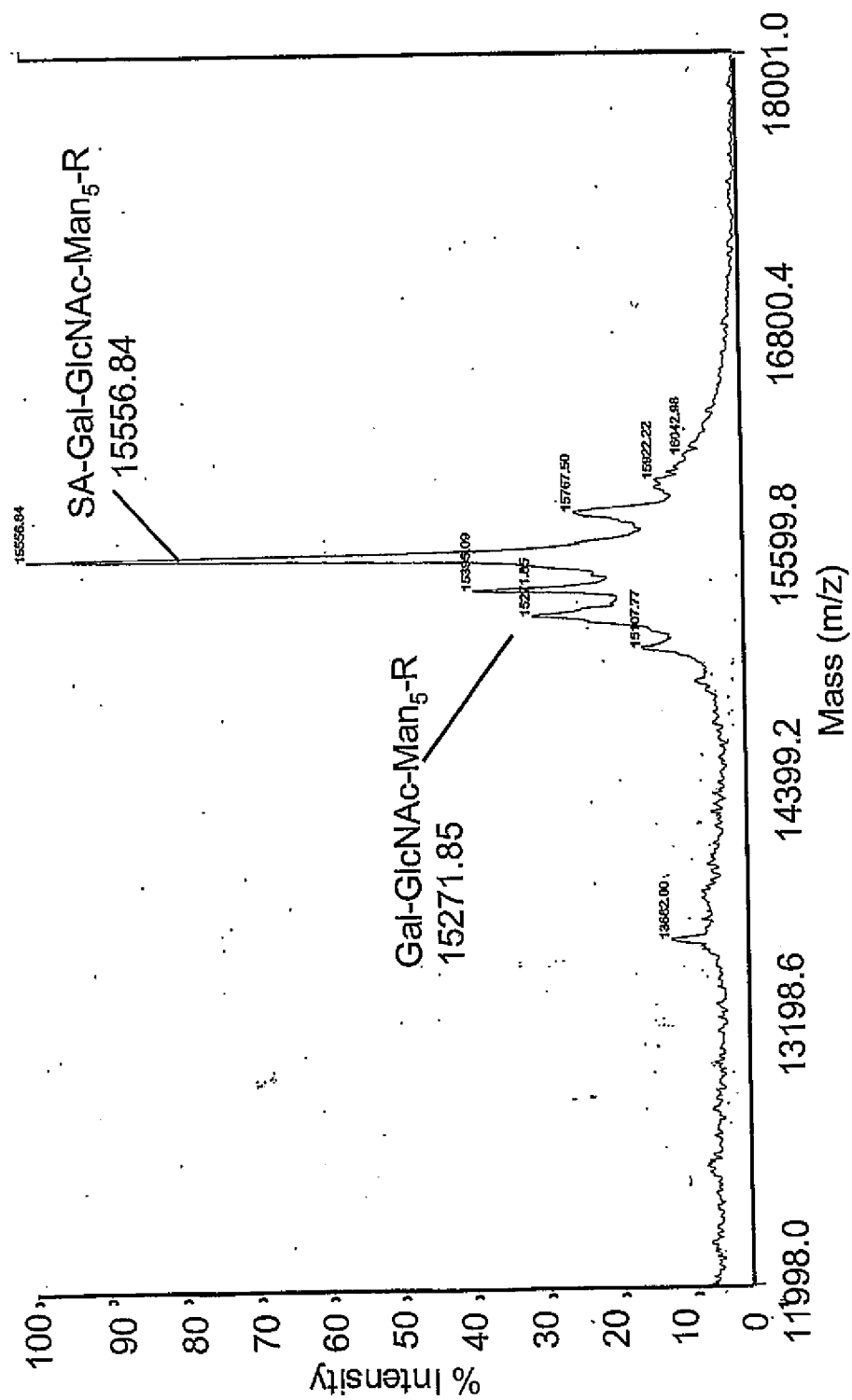


FIG. 98

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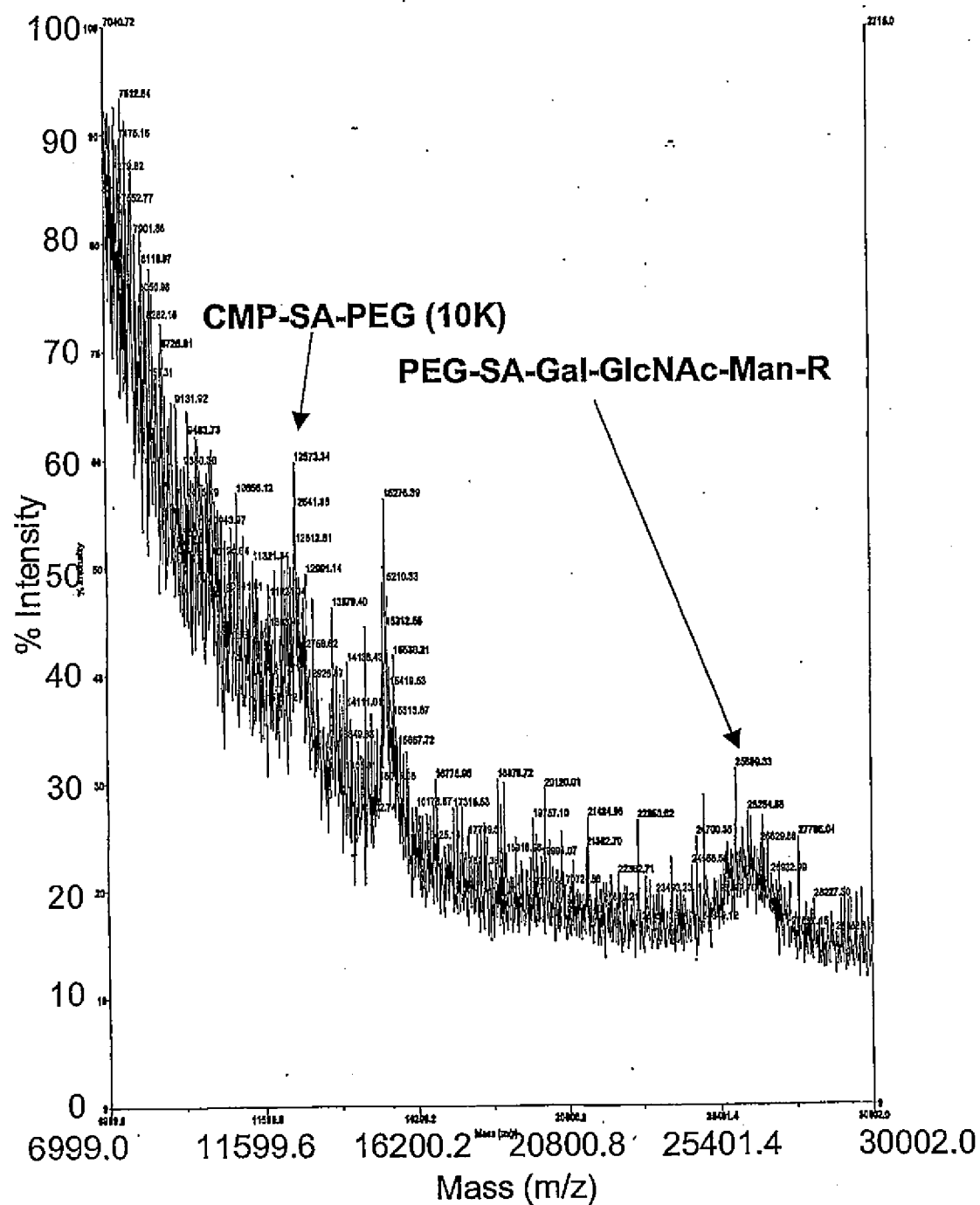
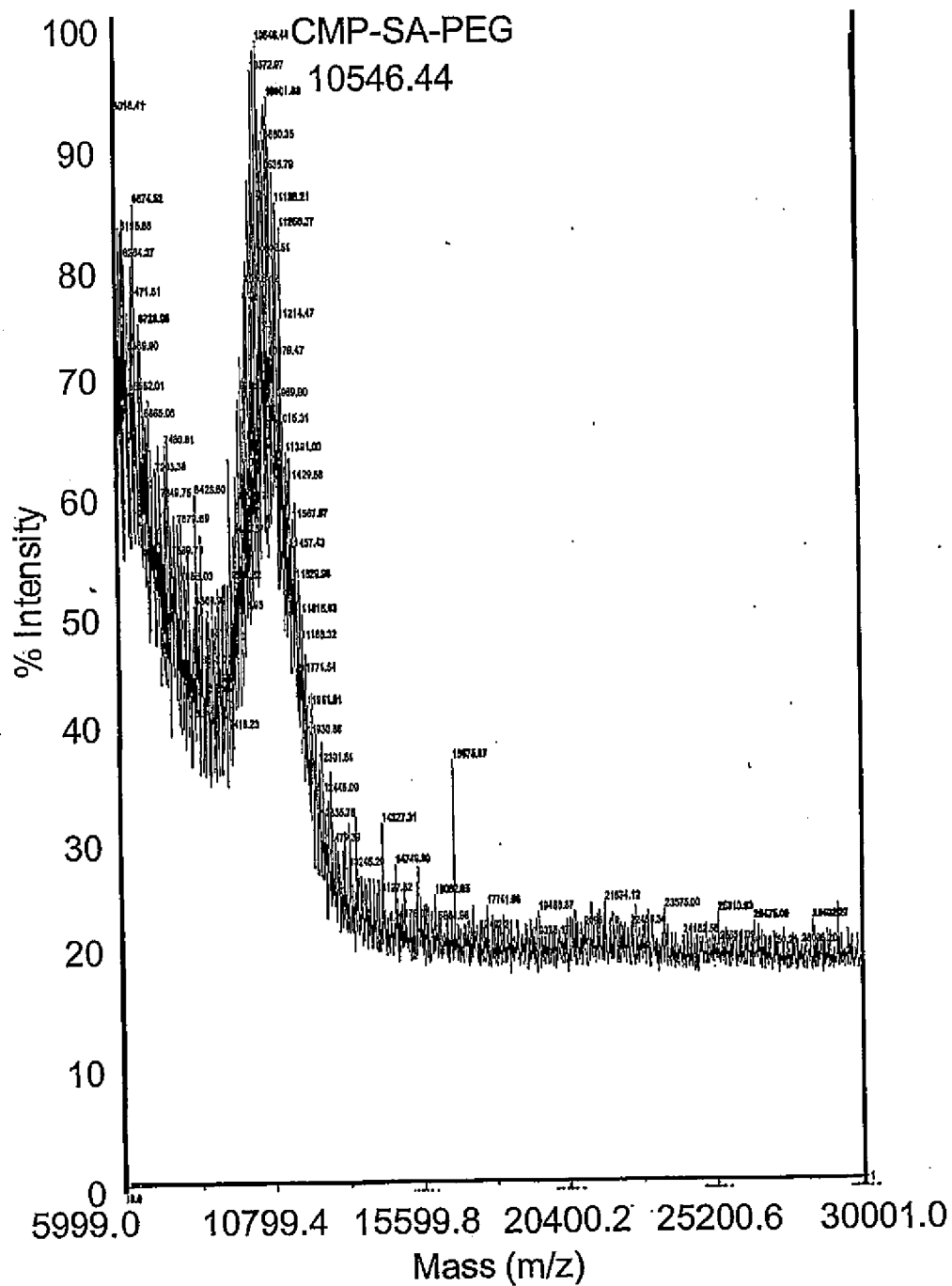


FIG. 99A

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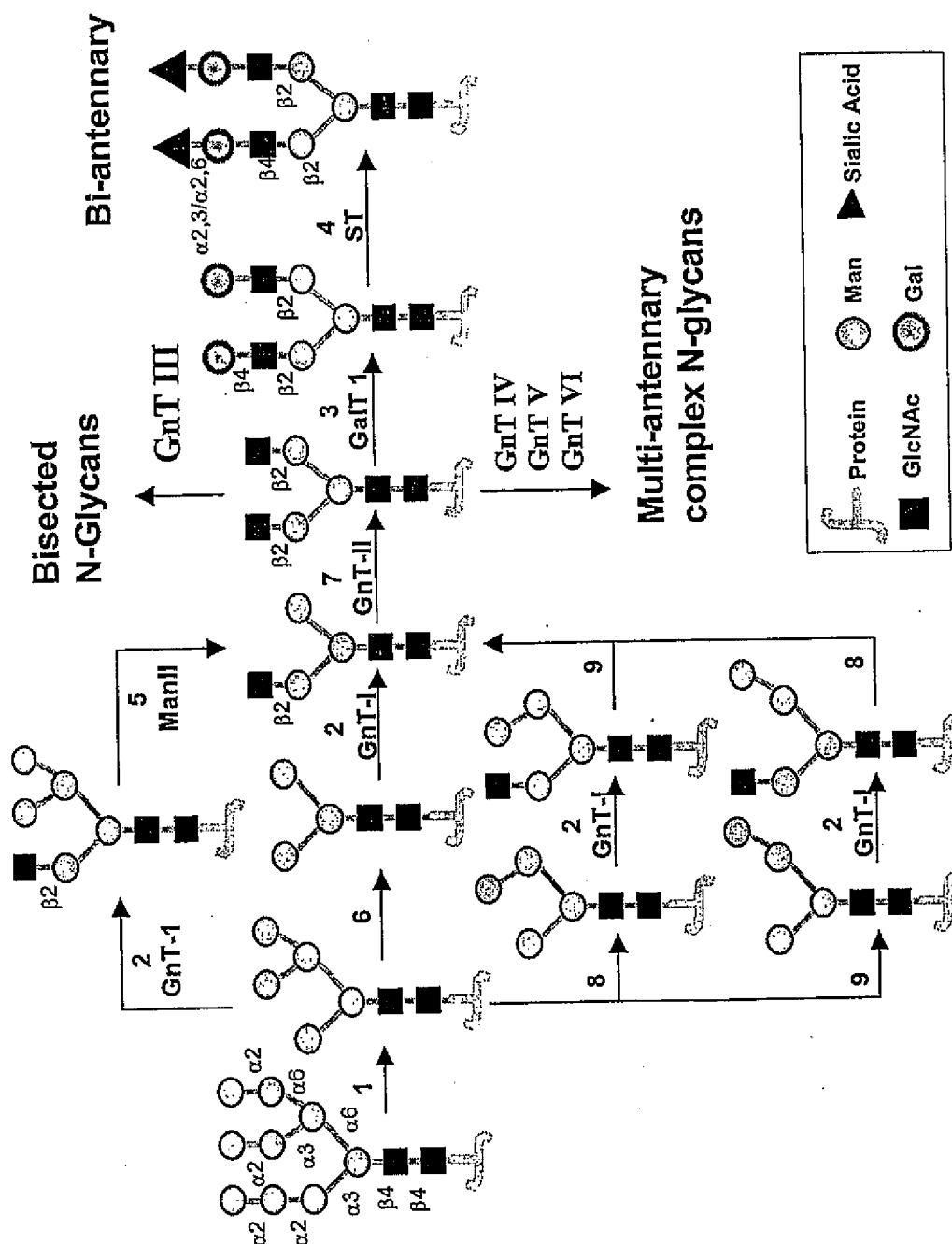


FIG. 100

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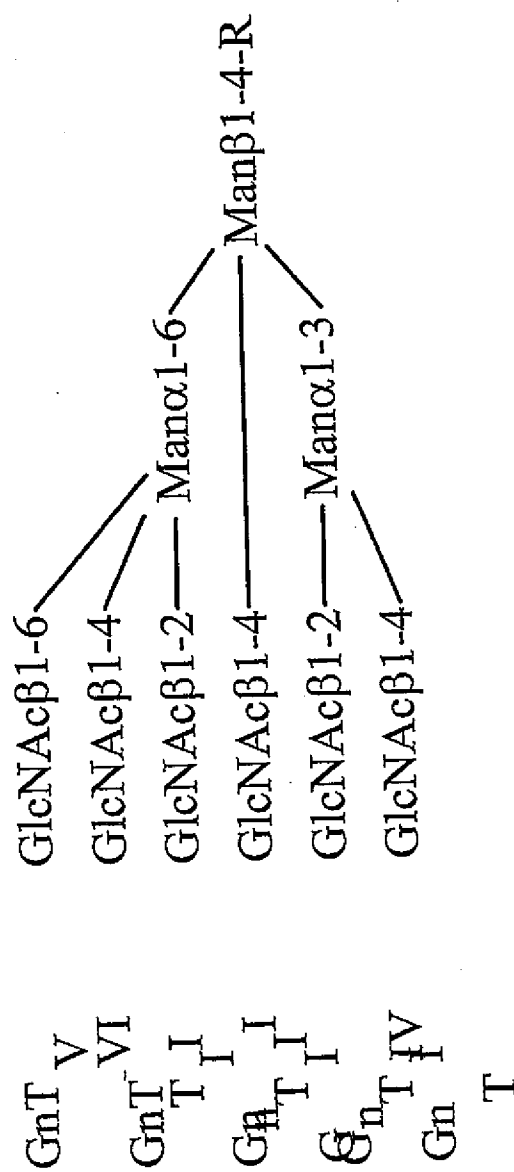


FIG. 101

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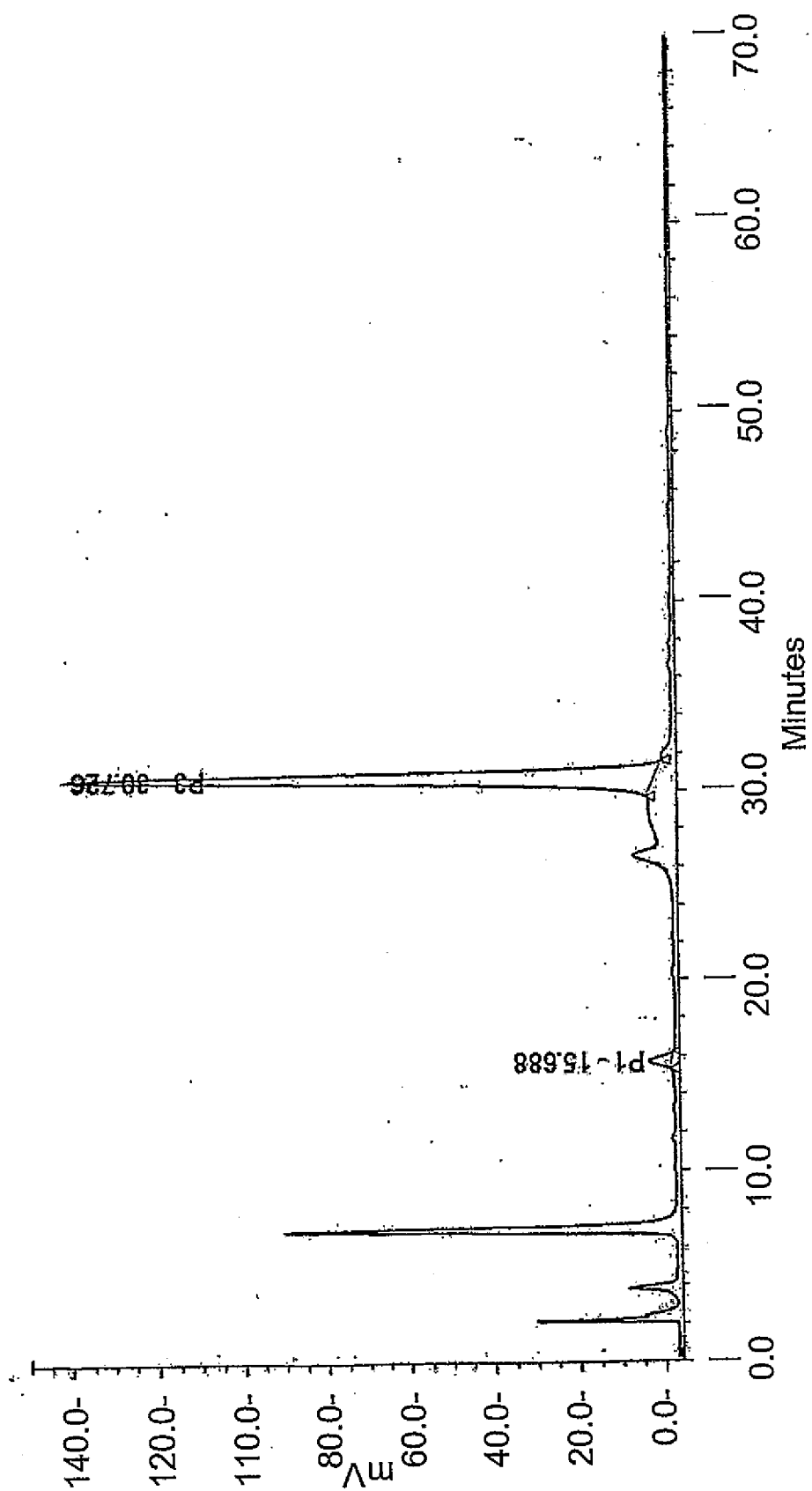


FIG. 102A

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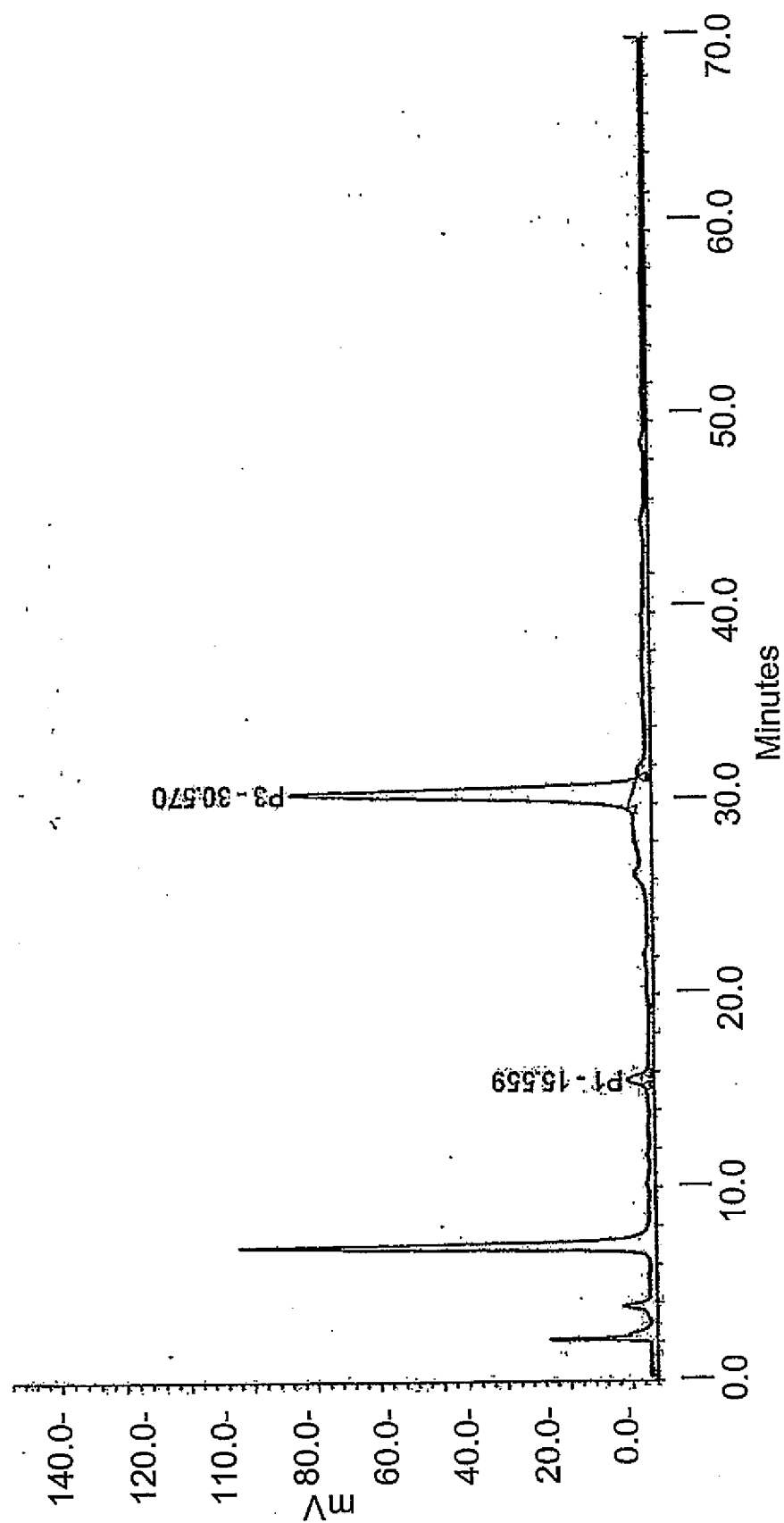


FIG. 102B

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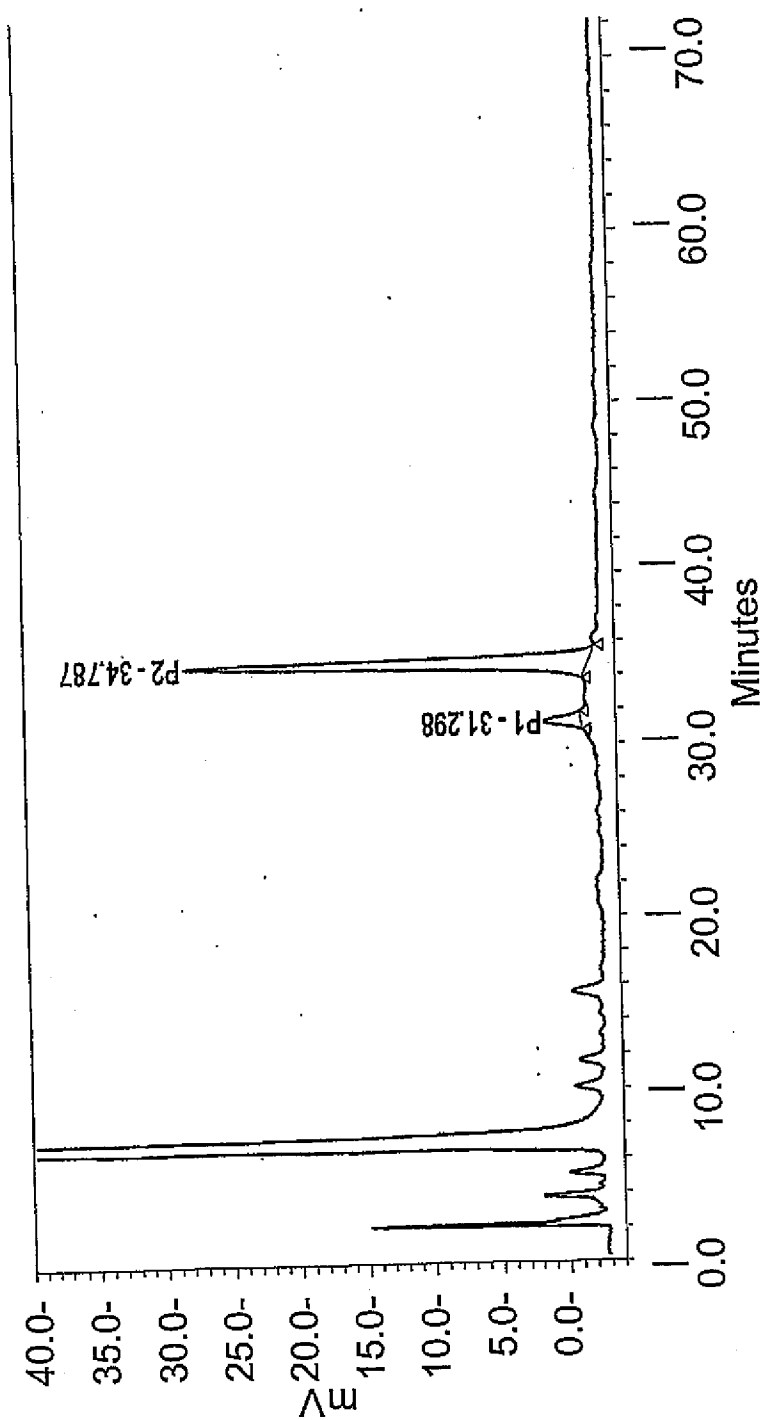


FIG. 103

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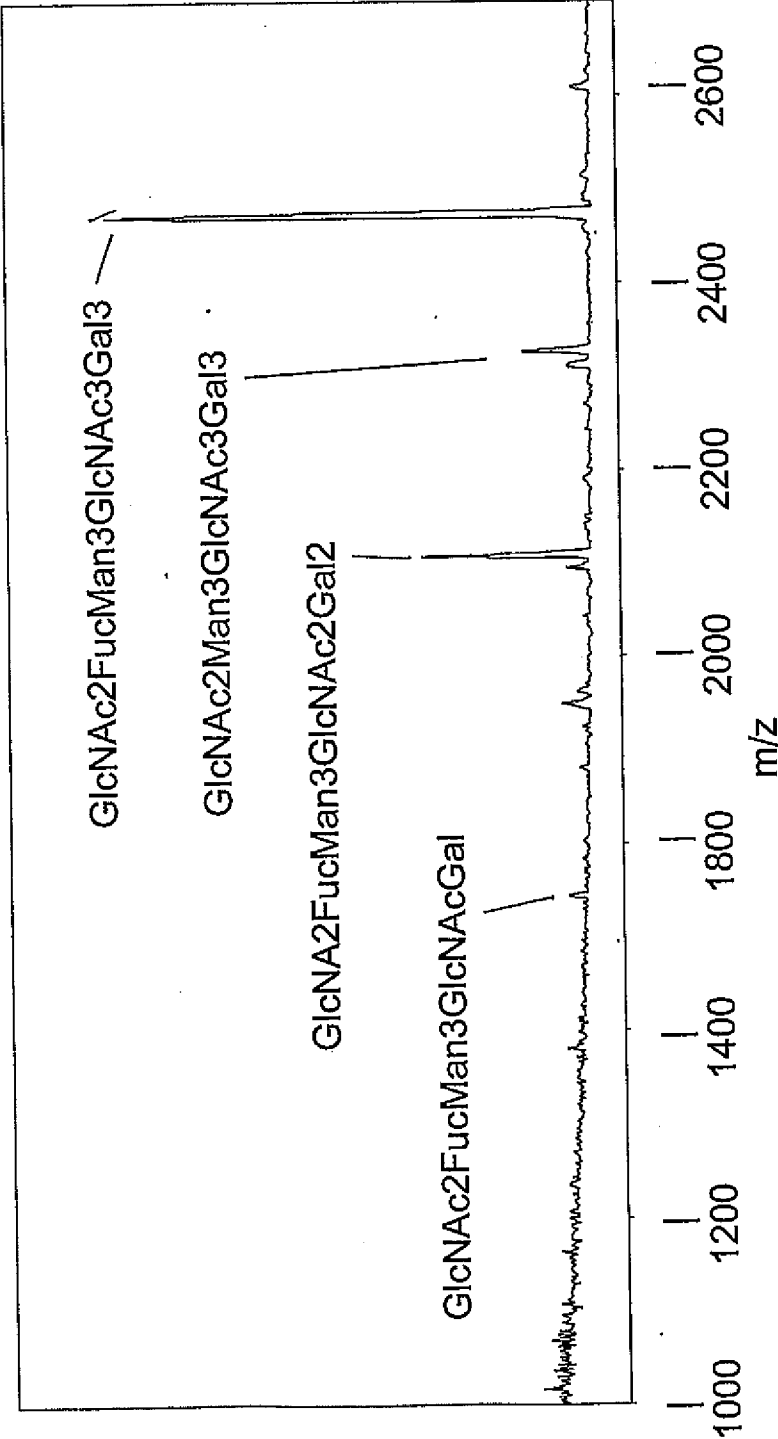


FIG. 104

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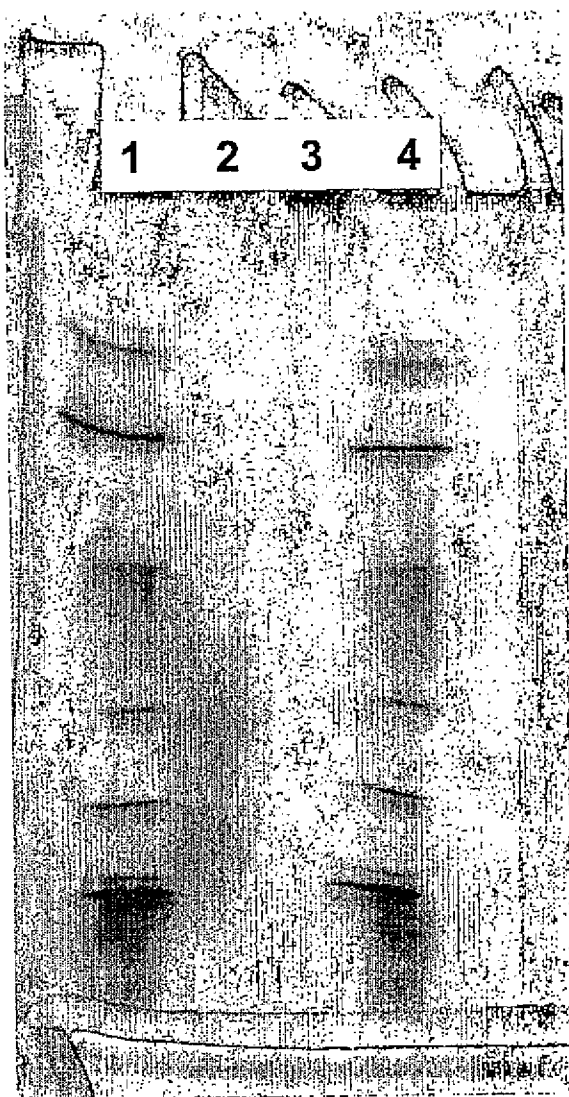


FIG. 105

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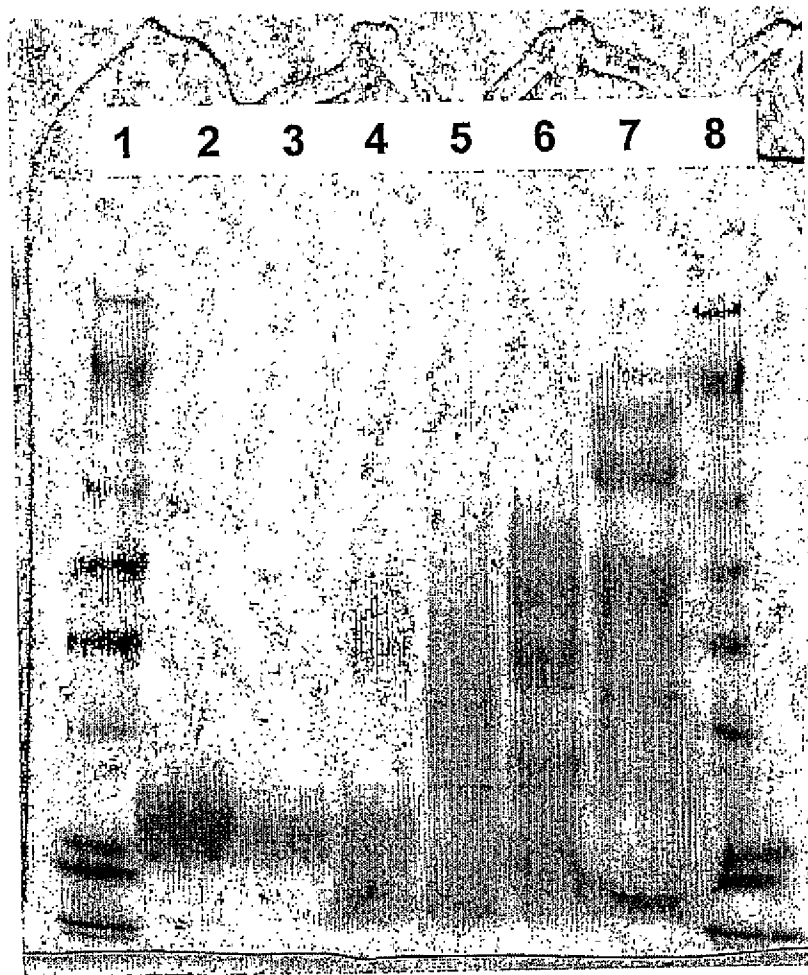


FIG. 106

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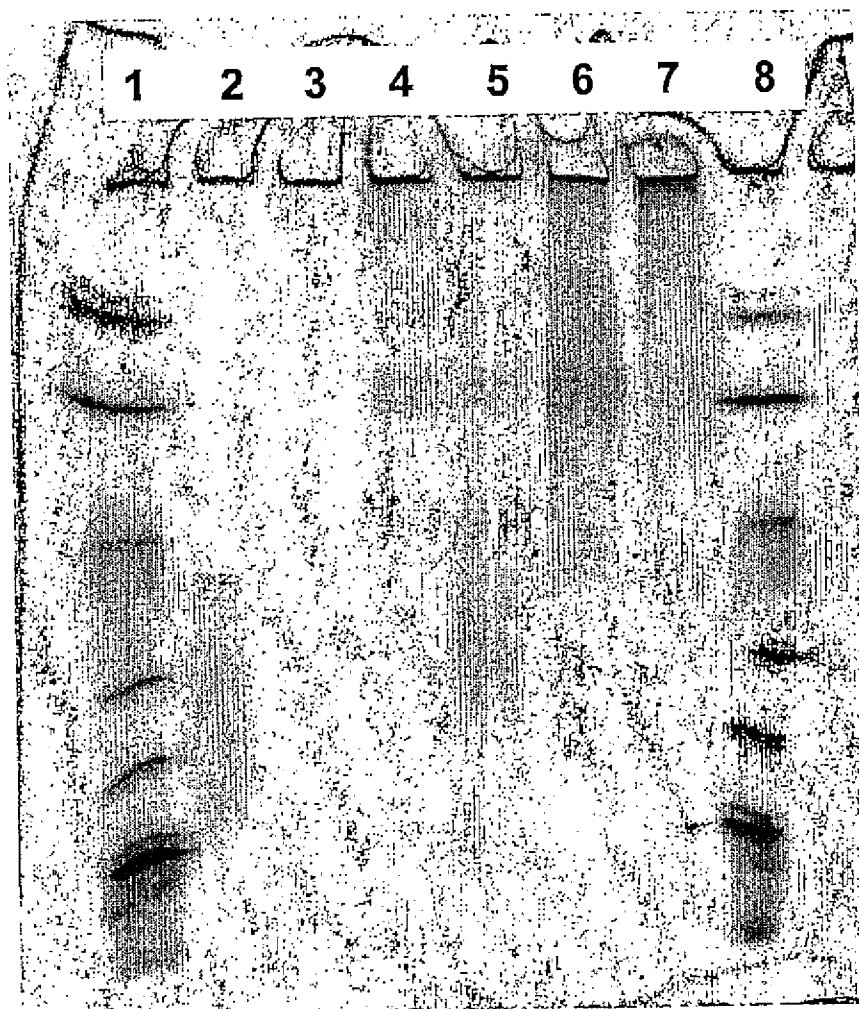


FIG. 107

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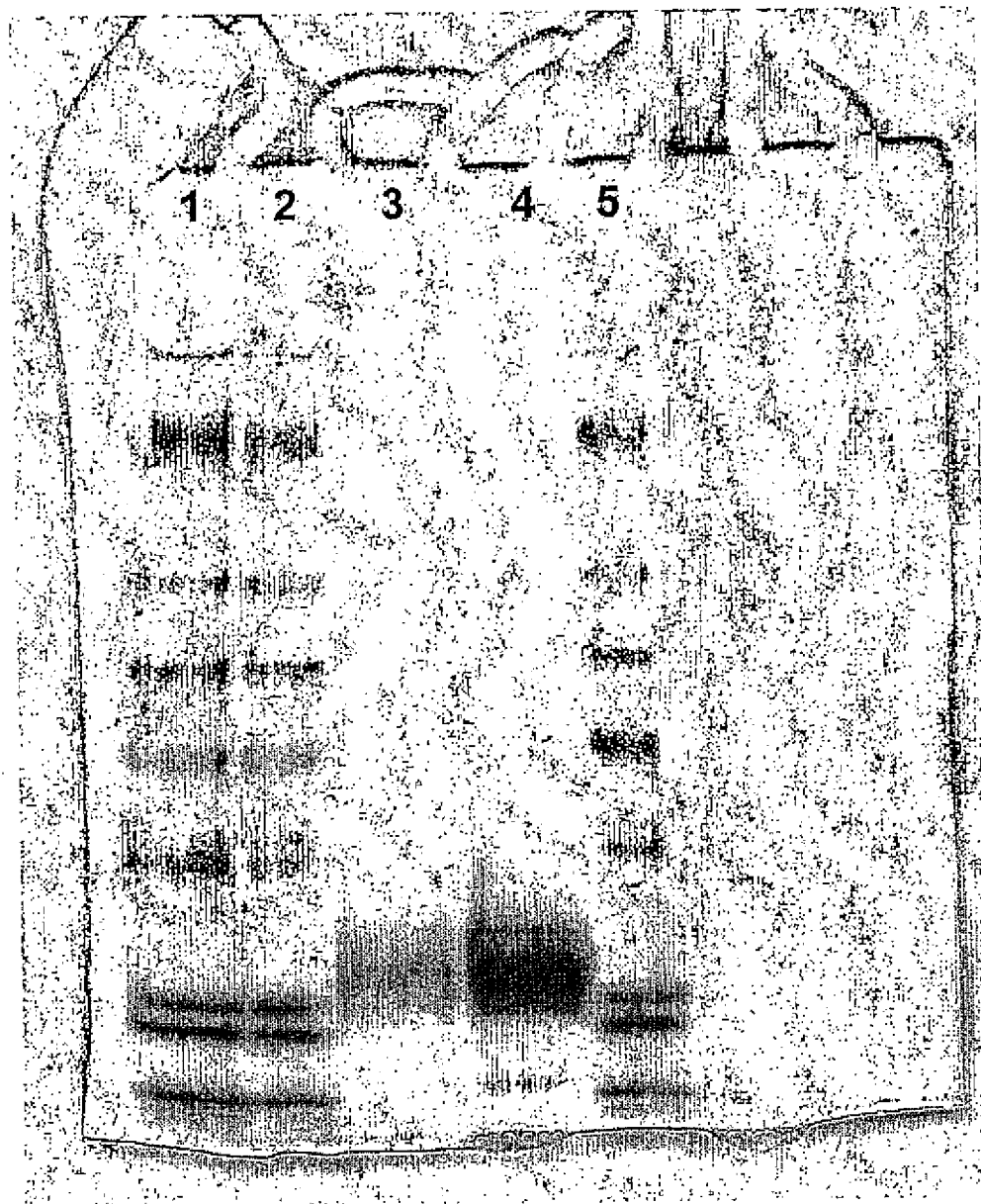


FIG. 108

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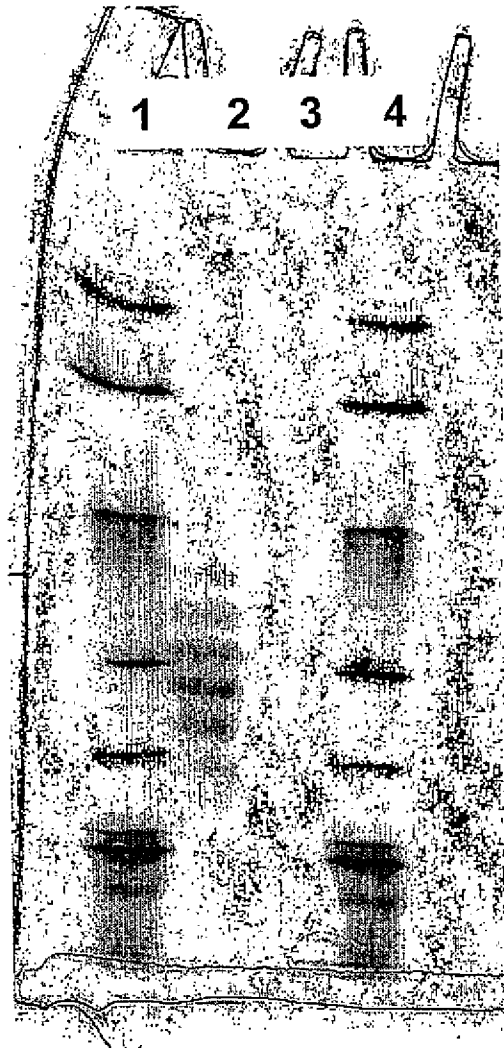


FIG. 109

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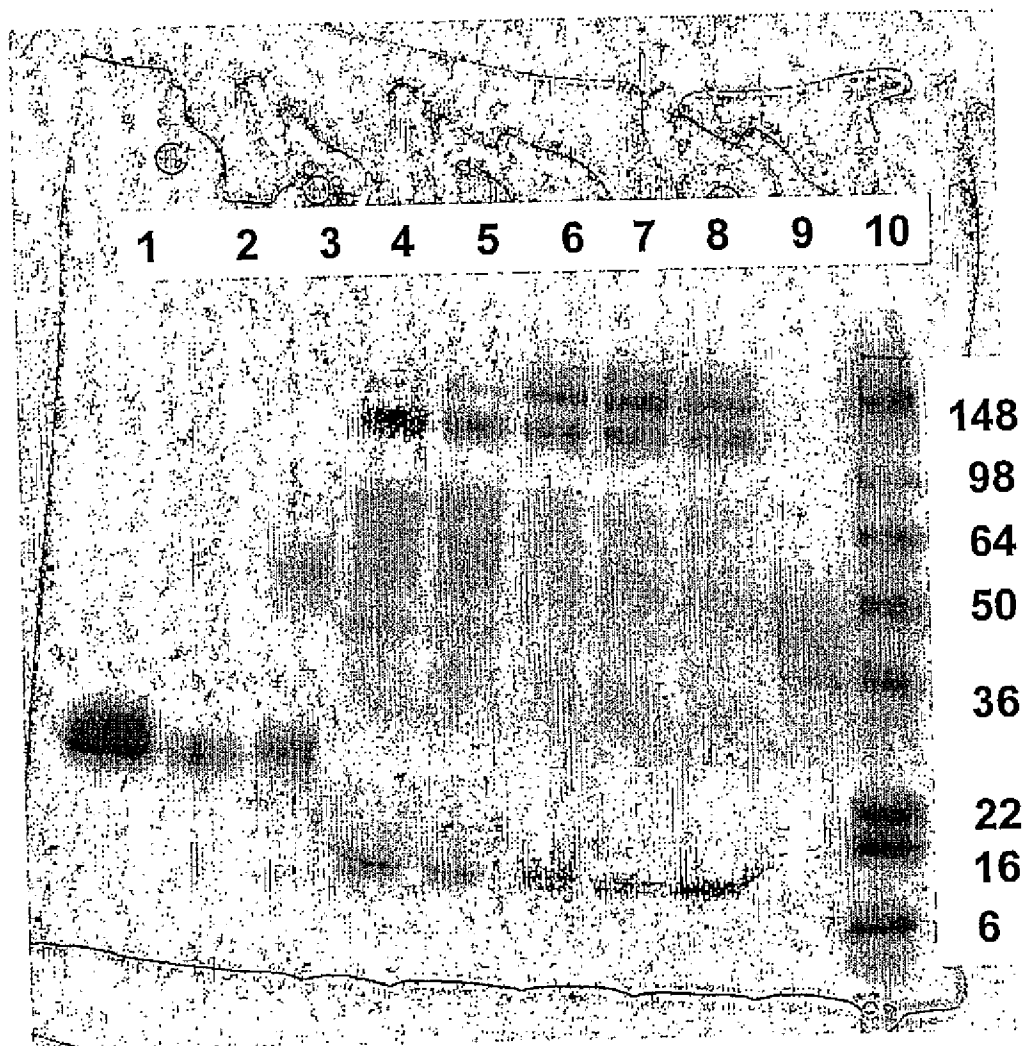


FIG. 110

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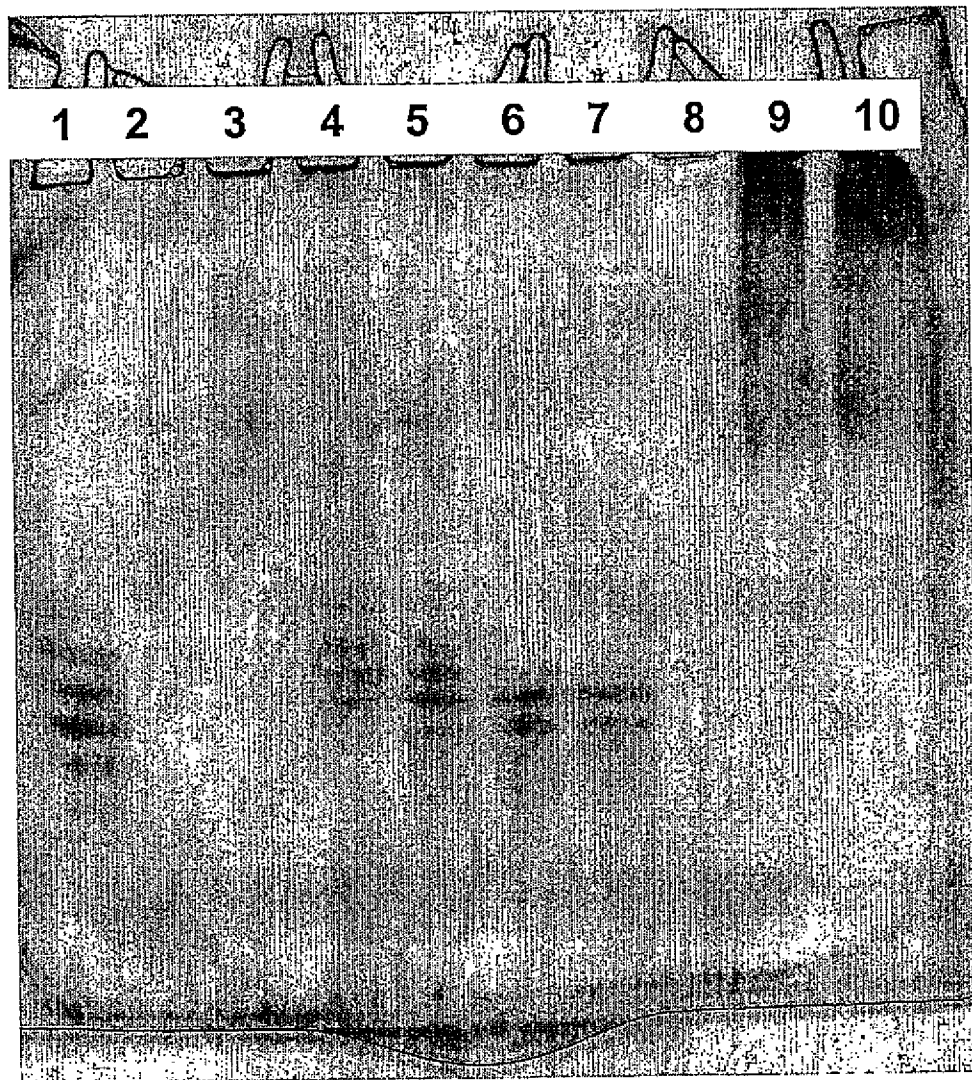


FIG. 111

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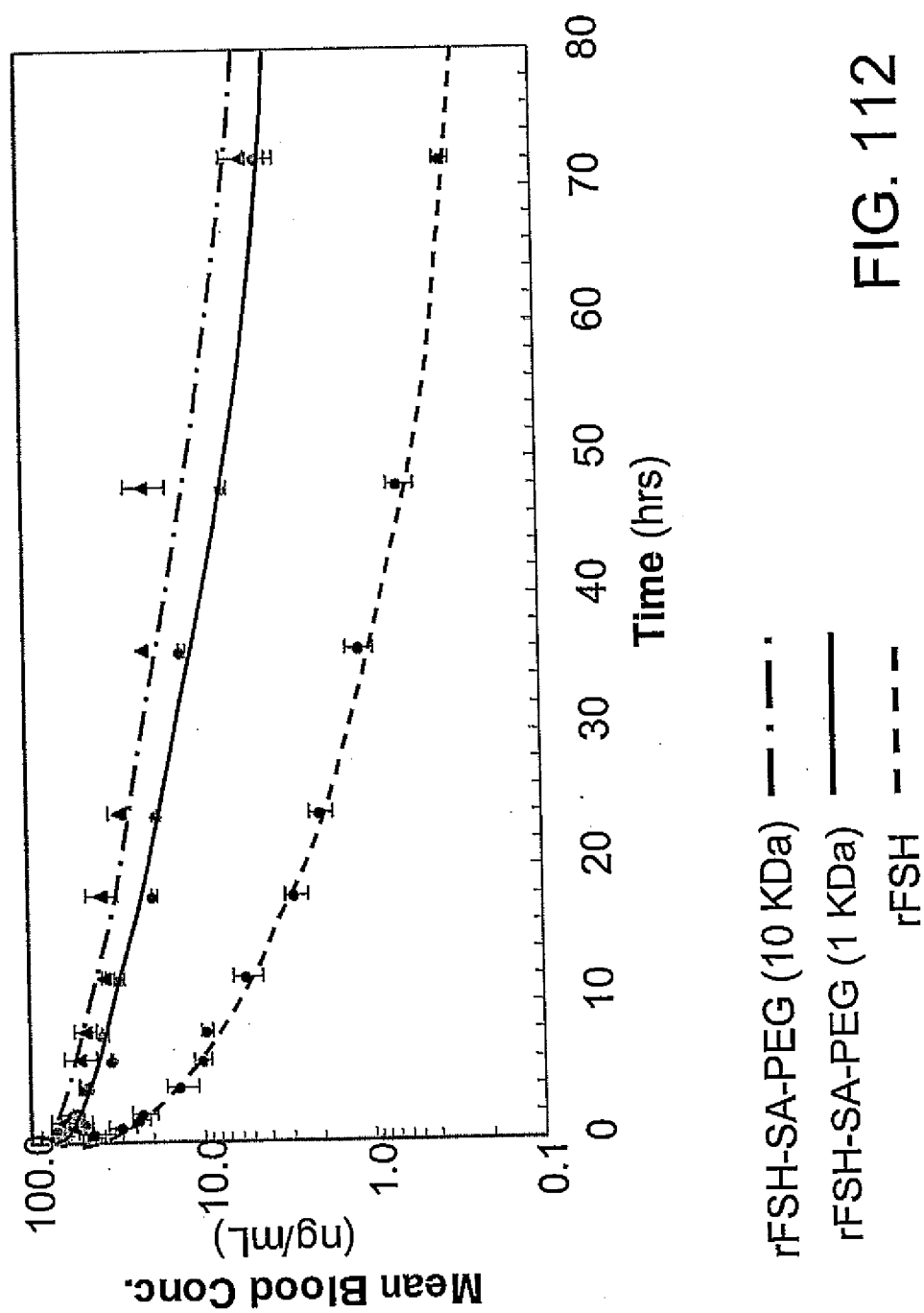


FIG. 112

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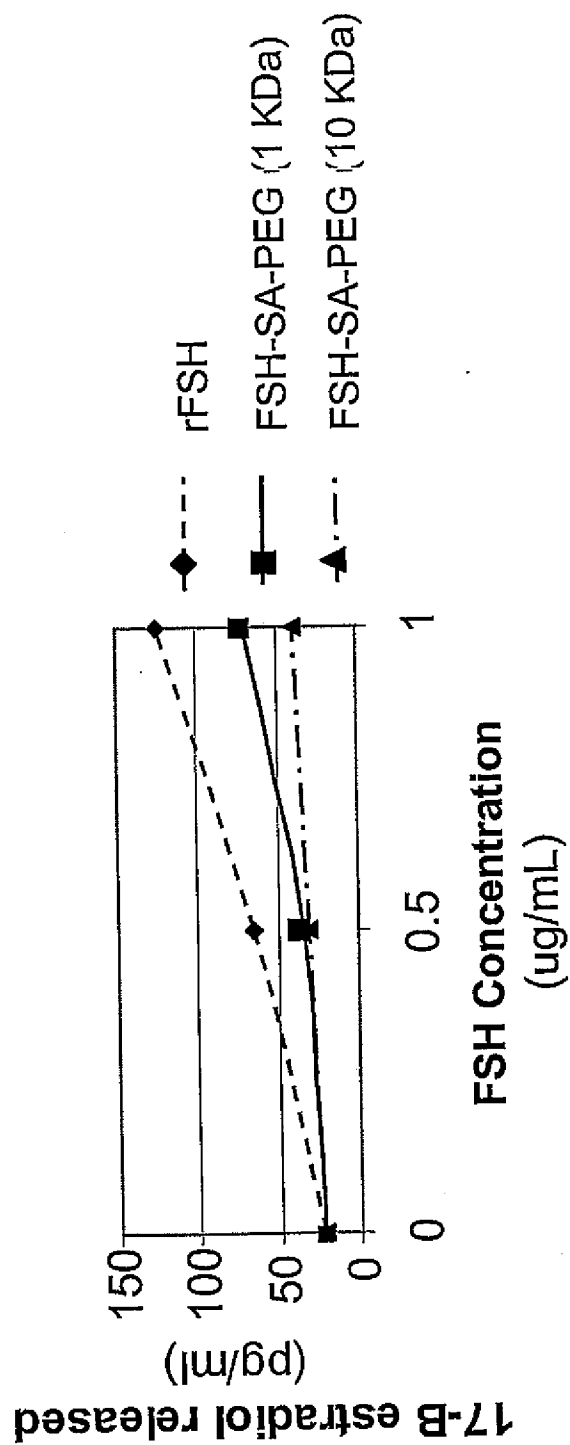


FIG. 113

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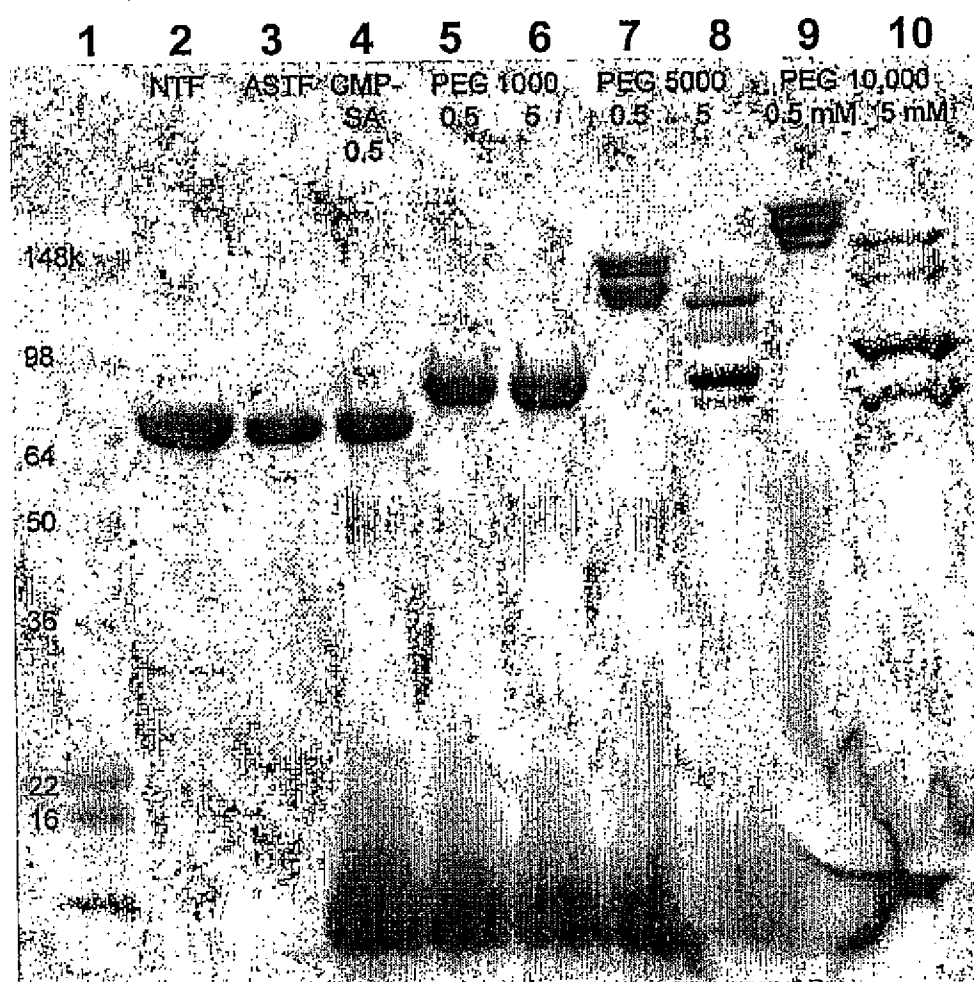


FIG. 114

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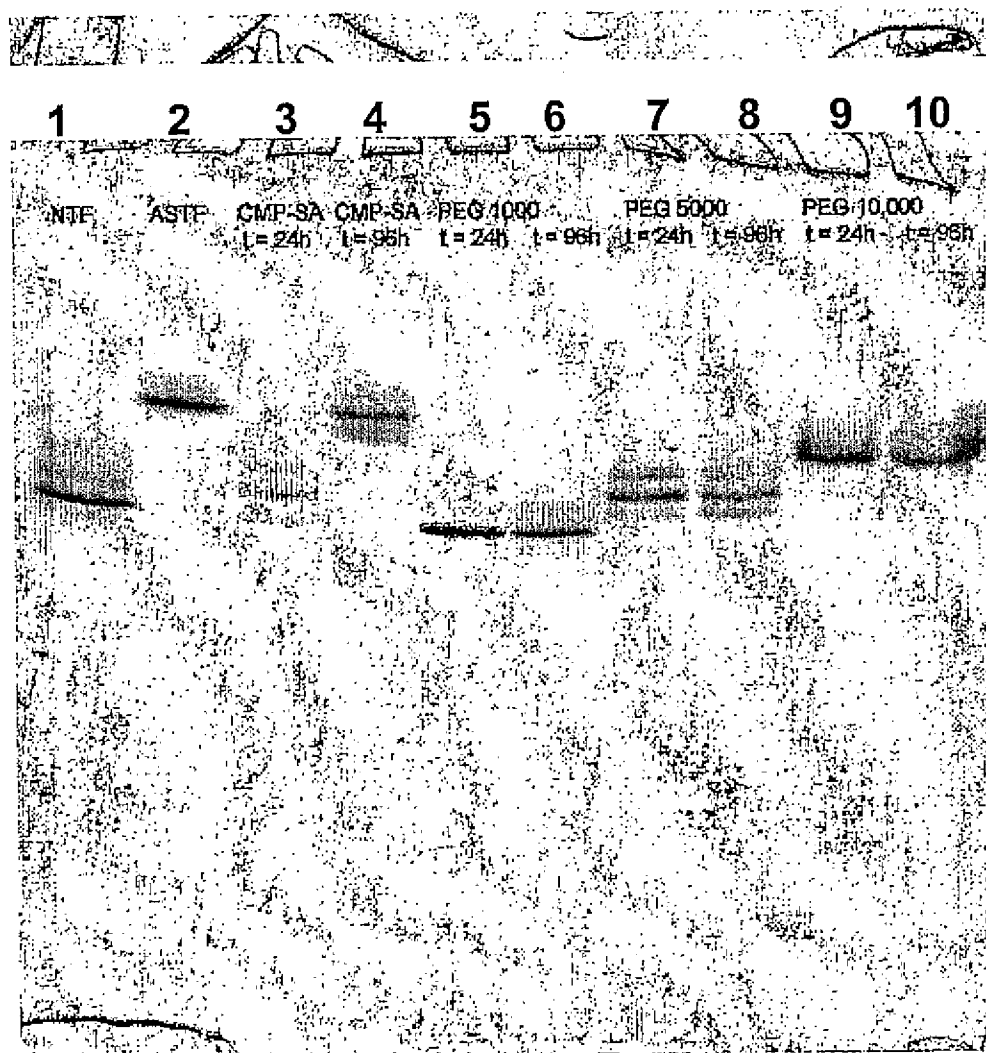


FIG. 115

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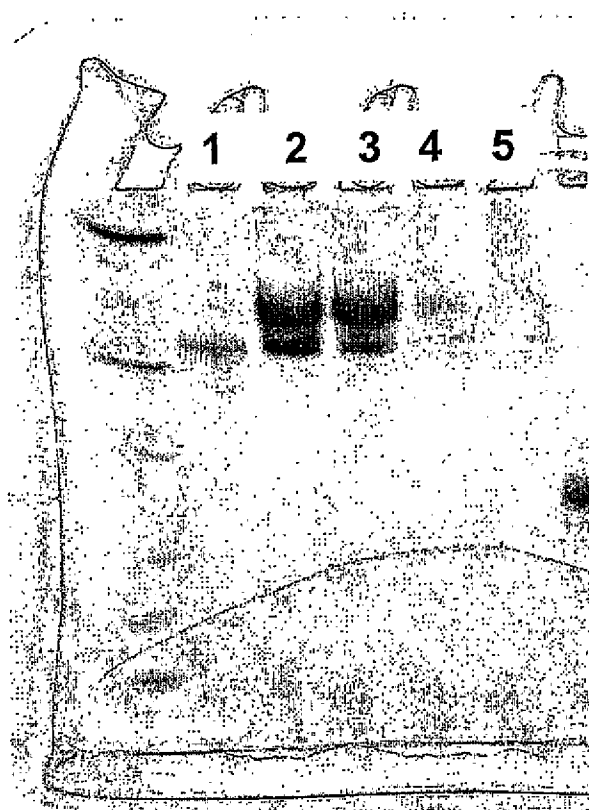


FIG. 116

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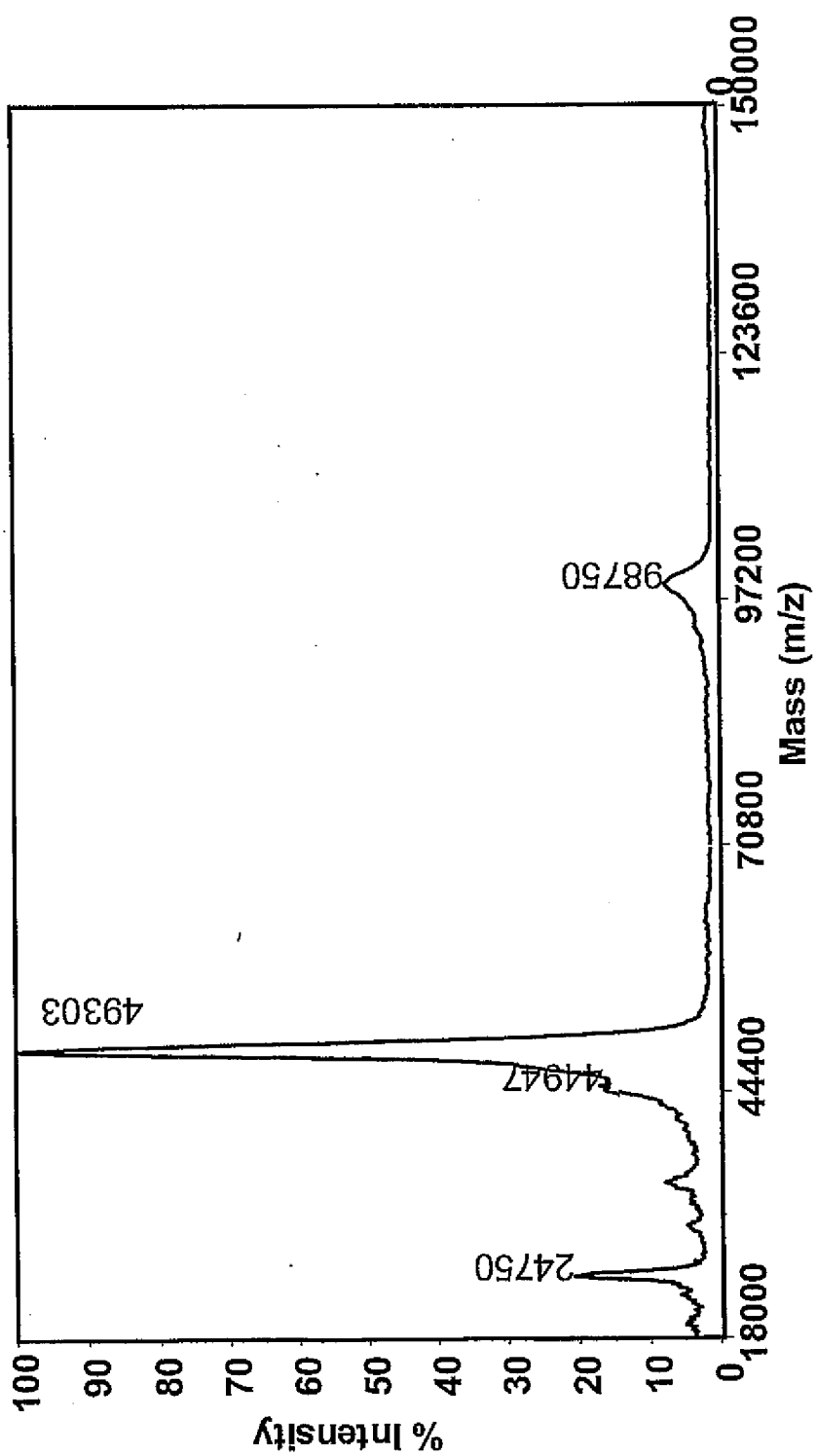


FIG. 117

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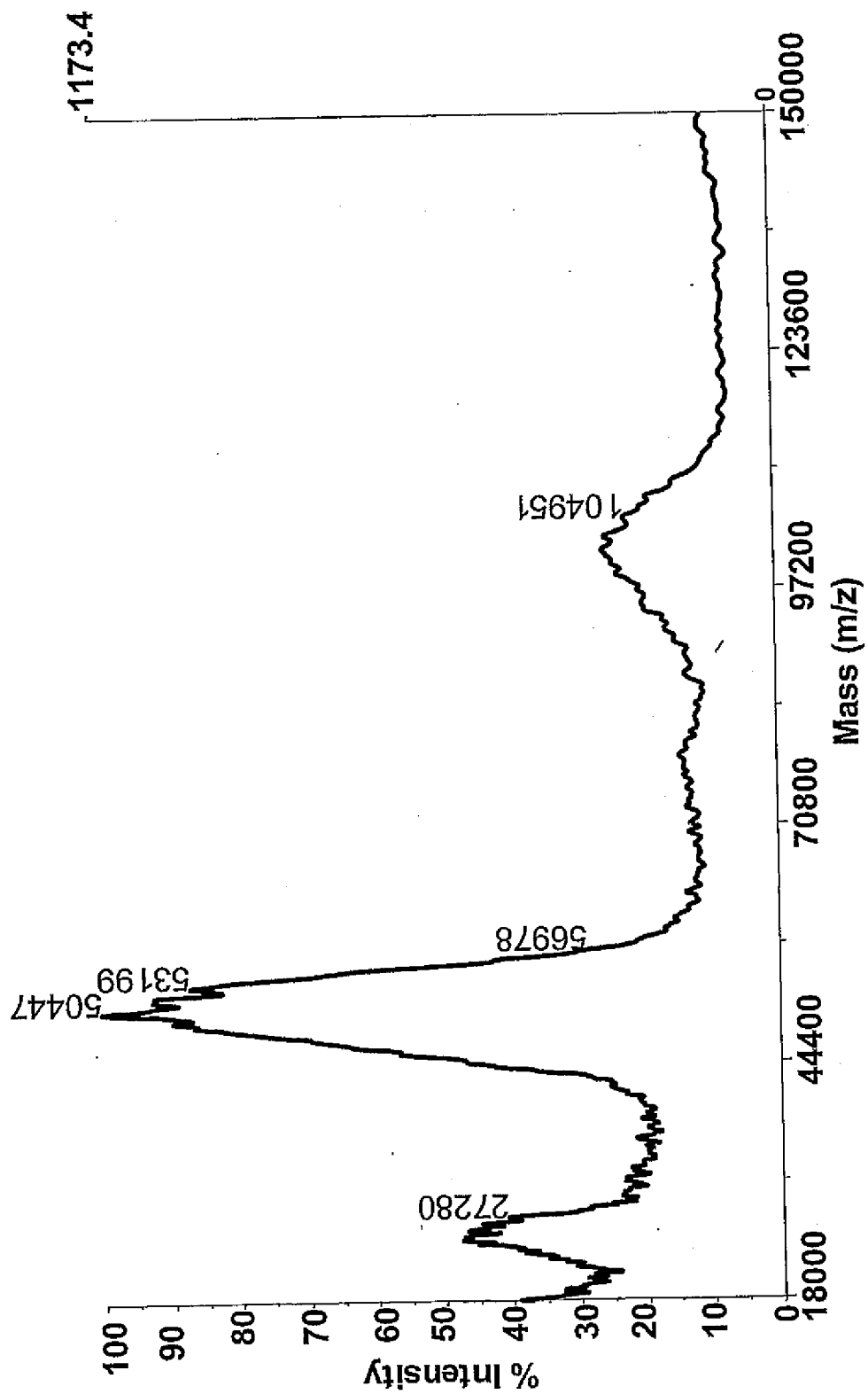


FIG. 118

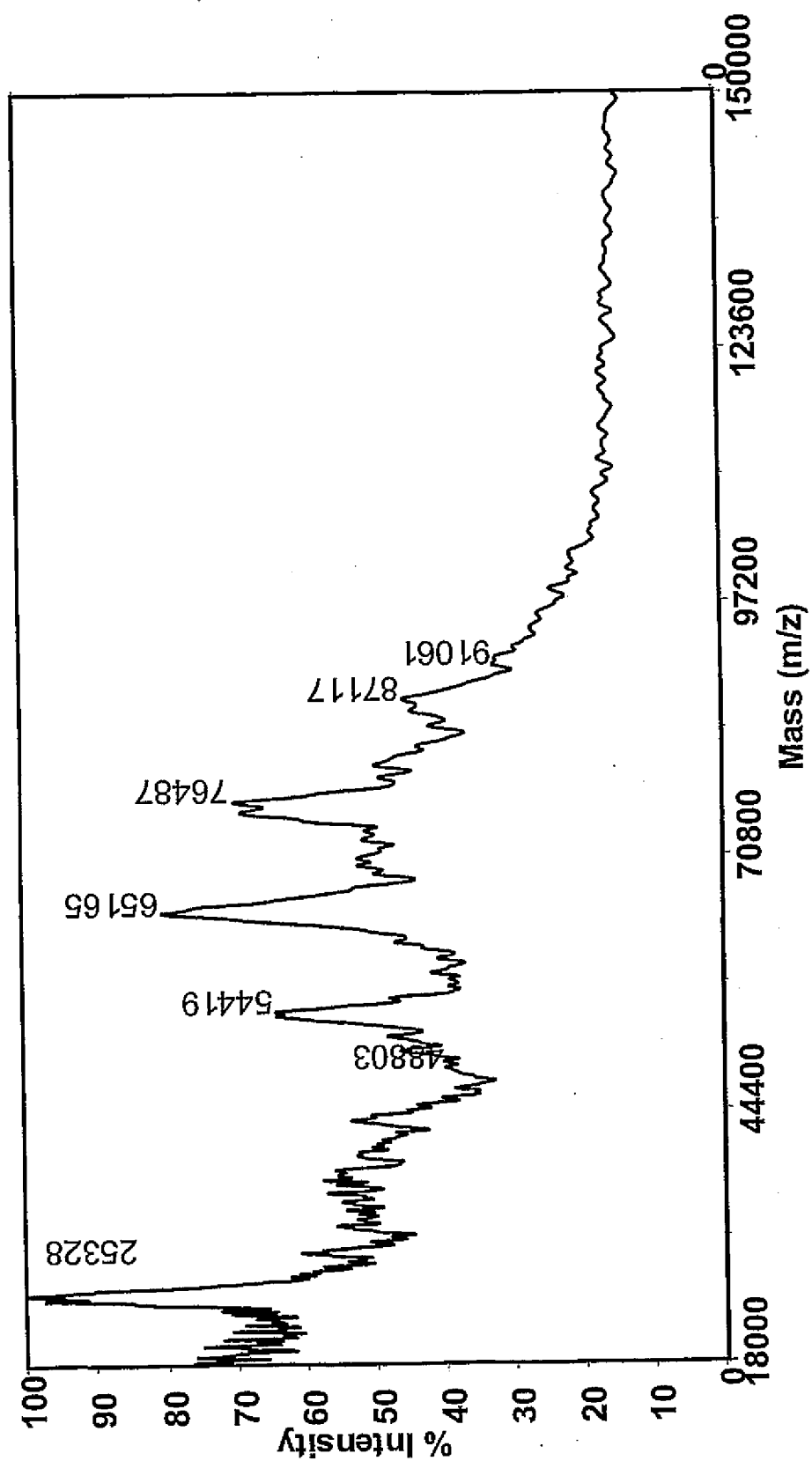


FIG. 119

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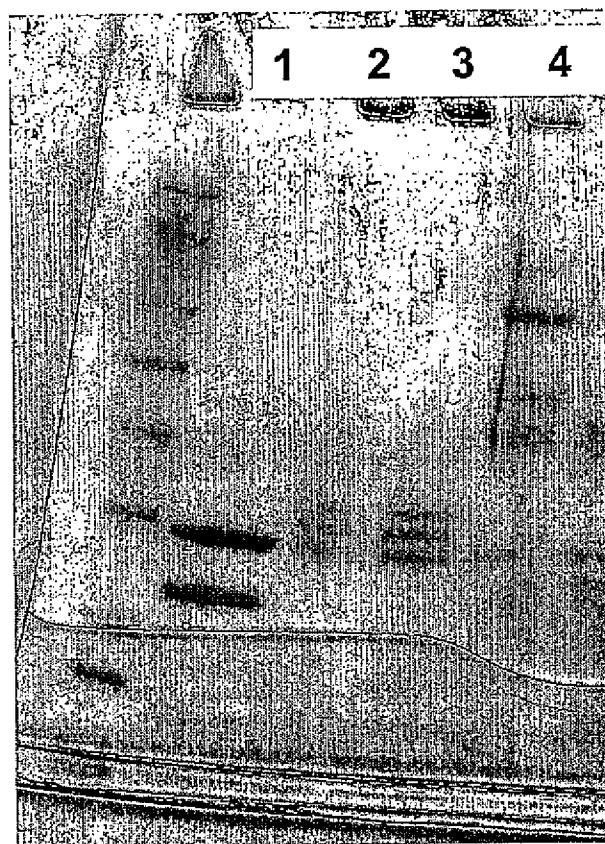


FIG. 120

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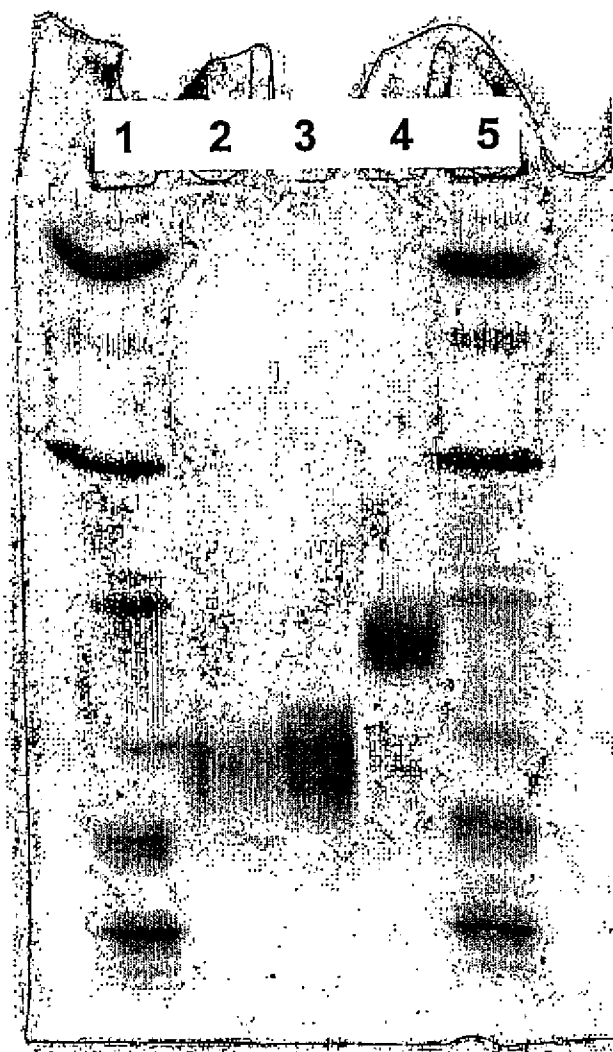


FIG. 121

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FIG. 122

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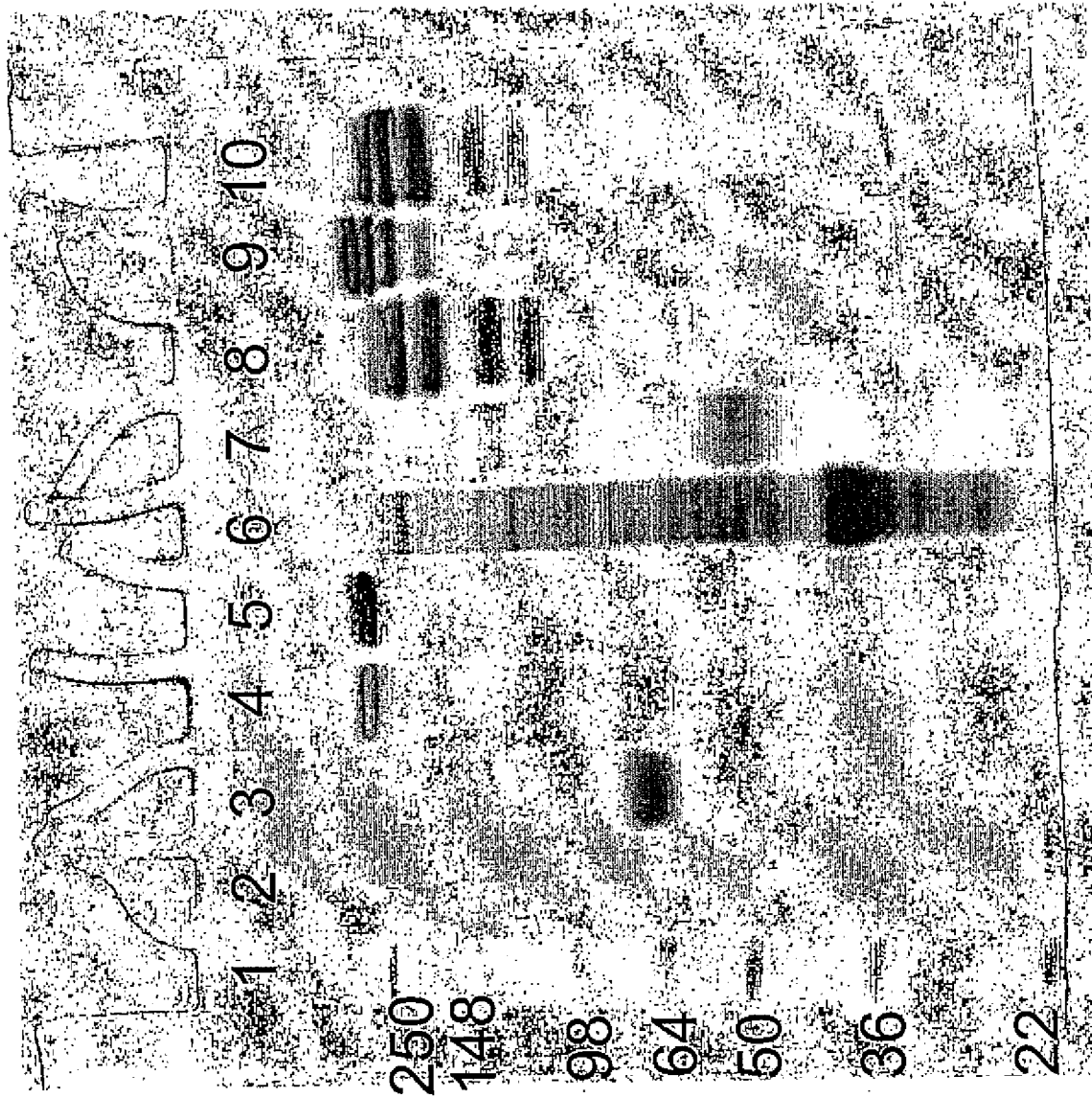


FIG. 123

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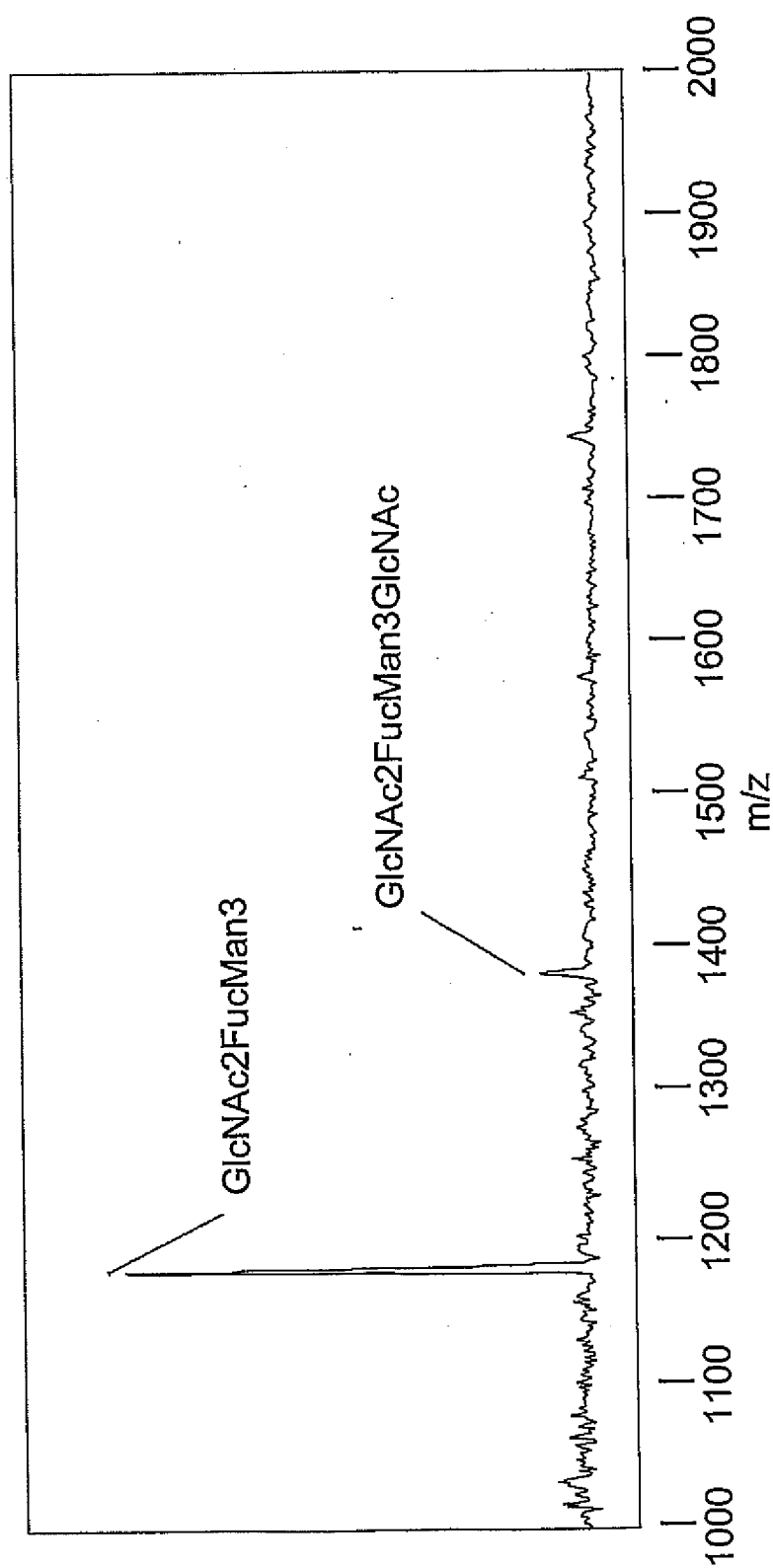


FIG. 124

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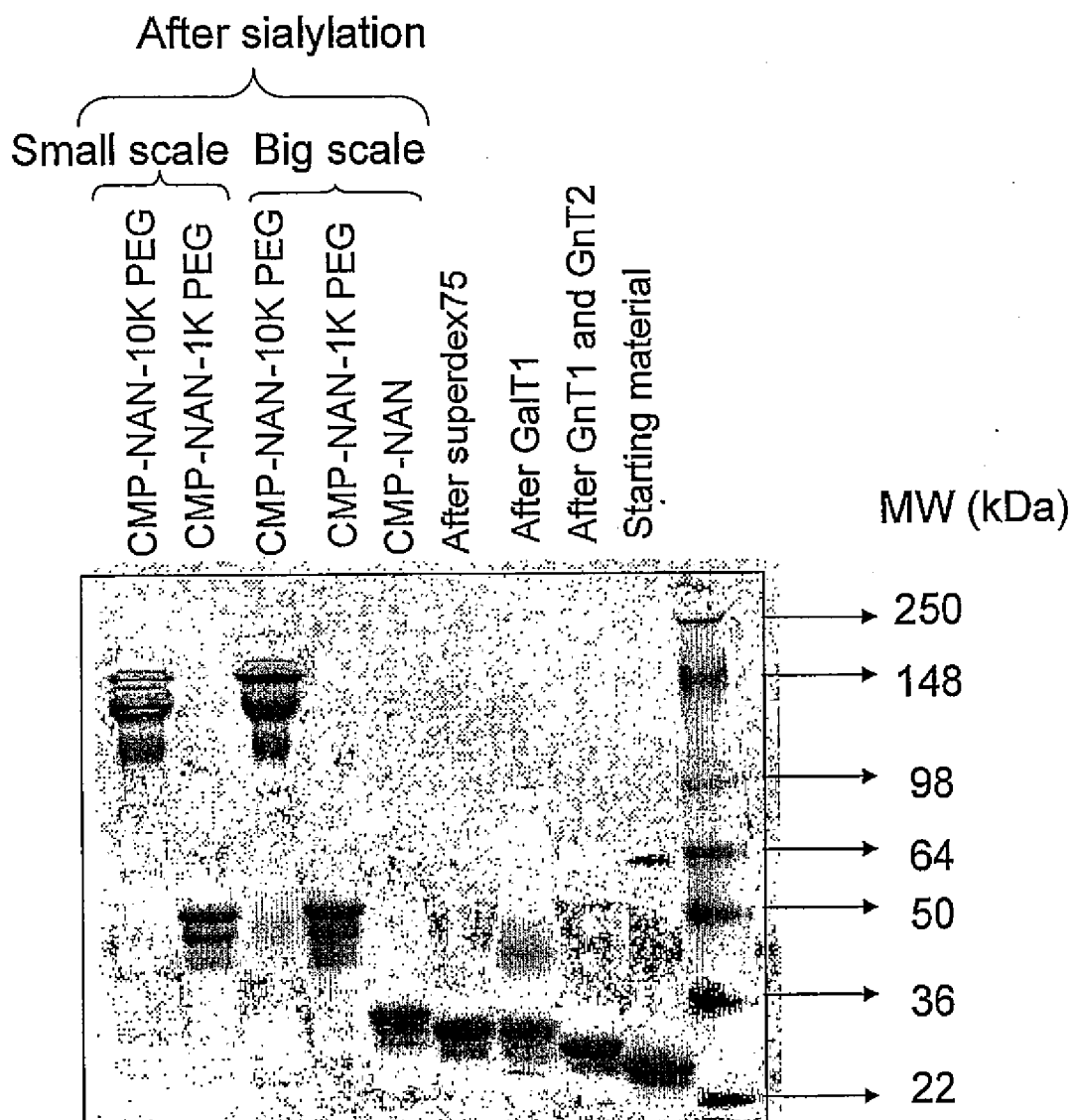


FIG. 125

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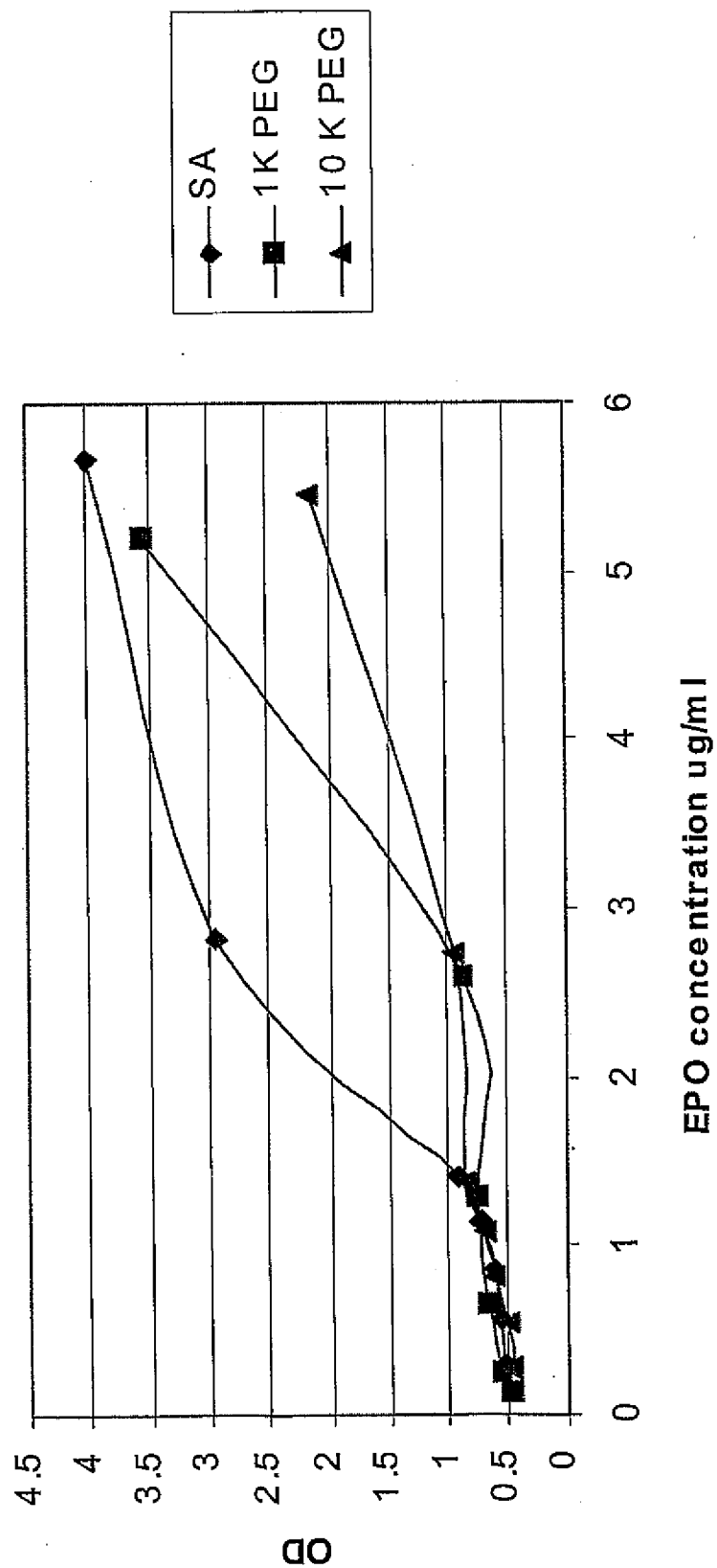


FIG. 126

SEQUENCE LISTING

<110> Neose Technologies, Inc.
 DeFrees, Shawn
 Zopf, David
 Bayer, Robert
 Bowe, Caryn
 Hakes, David
 Chen, Xi

<120> REMODELING AND GLYCOCONJUGATION OF PEPTIDES

<130> 040853-01-5050WO

<150> US 60/328,523

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 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140

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145

150

155

160

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Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
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```

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Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65          70          75          80

```

```

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
          85          90          95

```

```

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
          100          105          110

```

```

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
          115          120          125

```

```

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
          130          135          140

```

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 180 185

<210> 5
 <211> 757
 <212> DNA
 <213> Homo sapiens

<400> 5
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 ctctgttggc aattgaatgg gaggcttgaa tattgcctca aggacaggat gaactttgac 180
 atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc 240
 tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactgggtgg 300
 aatgagacta ttgttgagaa cctcctggct aatgtctatc atcagataaa ccatctgaag 360
 acagtcctgg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt 420
 ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt 480
 cactgtgcct ggaccatagt cagagtggaa atcctaagga acttttactt cattaacaga 540
 cttacaggtt acctccgaaa ctgaagatct cctagcctgt ccctctggga ctggacaatt 600
 gcttcaagca ttcttcaacc agcagatgct gtttaagtga ctgatggcta atgtactgca 660
 aatgaaagga cactagaaga ttttgaaatt tttattaaat tatgagttat ttttatttat 720
 ttaaatttta ttttggaaaa taaattattt ttggtgc 757

<210> 6
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
 1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 180 185

<210> 7
 <211> 1332
 <212> DNA
 <213> Homo sapiens

<400> 7
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 gcggttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180
 tccttcgagg aggcccgga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaattggggg ctccctgcaag 300
 gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggcog gaactgtgag 360
 acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc 420
 agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca 480
 gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa 540
 aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg 600
 gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg 660
 atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg 720
 aacctgatcg cgggtgctggg cgagcacgac ctccagcagc acgacgggga tgagcagagc 780
 cggcggtgtg cgaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac 840
 atgcgctgc tccgcctgca ccagcccggtg gtccctactg accatgtggt gcccctctgc 900
 ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc 960
 ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt gctcaacgtg 1020
 ccccggtga tgaccagga ctgcctgcag cagtcaaggga aggtgggaga ctccccaaat 1080
 atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg 1140
 gacagtggag gccacatgc caccactac cggggcacgt ggtacctgac gggcatcgtc 1200
 agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag 1260
 tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gccaggagt cctcctgcga 1320
 gcccatttc cc 1332

<210> 8
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 8

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
 1 5 10 15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
 20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
 35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
 50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
 85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
 100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
 115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
 130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
 145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
 165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
 435 440

<210> 9
 <211> 1437
 <212> DNA
 <213> Homo sapiens

<400> 9
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 ggatatctac tcagtgtga atgtacagtt tttcttgatc atgaaaacgc caacaaaatt 120
 ctgaatcggc caaagaggta taattcaggt aaattggaag agtttggtca aggggaacott 180

gagagagaat gtatggaaga aaagtgtagt tttgaagaac cactgagaagt ttttgaaaac 240
 actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat 300
 ccatgtttta atggcggcag ttgcaaggat gacattaatt cctatgaatg ttggtgtccc 360
 tttggatttg aaggaaagaa ctgtgaatta gatgtaacat gtaacattaa gaatggcaga 420
 tgcgagcagt tttgtaaaaa tagtgctgat aacaagggtg tttgctcctg tactgagggg 480
 tatcgacttg cagaaaacca gaagtcctgt gaaccagcag tgccatttcc atgtggaaga 540
 gtttctgttt cacaaacttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac 600
 tatgtaaaac ctactgaagc tgaaaccatt ttggataaca tcaactcaagg cacccaatca 660
 tttaatgact tcaactcgggt tgttggtgga gaagatgcc aaccagggtca attcccttgg 720
 caggttgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780
 tggattgtaa ctgctgcccc ctgtgttgaa actgggtgta aaattacagt tgcgcaggt 840
 gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tcgagcaatt 900
 attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccttctg 960
 gaactggacg aacccttagt gctaaacagc tacgttacac ctatttgcac tgctgacaag 1020
 gaatacacga acatcttcct caaatttggg tctggctatg taagtggctg ggcaagagtc 1080
 ttccacaaag ggagatcagc tttagttctt cagtacctta gagttccact tgttgaccga 1140
 gccacatgtc ttgatctac aaagttcacc atctataaca acatgttctg tgctggcttc 1200
 catgaaggag gtagagattc atgtcaagga gatagtgggg gaccccatgt tactgaagtg 1260
 gaagggacca gtttcttaac tggaattatt agctggggtg aagagtgtgc aatgaaaggc 1320
 aaatatggaa tatataccaa ggtatccogg tatgtcaact ggattaagga aaaaacaaag 1380
 ctcaactaat gaaagatgga ttccaaggt taattcattg gaattgaaaa ttaacag 1437

<210> 10
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
 1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
 20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
 50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn
 65 70 75 80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
 85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
 100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
 115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
 130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
 145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
 165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu
 195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe
 210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
 225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
 245 250 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His
 290 295 300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu
 305 310 315 320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys
 325 330 335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
 340 345 350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu
 355 360 365

Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu
 370 375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11
 <211> 603
 <212> DNA
 <213> Homo sapiens

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<400> 11
atggattact acagaaaata tgcagctatc tttctgggtca cattgtcggg gtttctgcat      60
gttctccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccda      120
ttctttctccc agccgggtgc cccaatactt cagtgcattgg gctgctgctt ctctagagca      180
tatcccactc cactaagggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag      240
tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg      300
gagaaccaca cggcgtgccca ctgcagtact tgttattatc acaaatctta aatgttttac      360
caagtgtgtg cttgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt      420
atggcttttg gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg      480
atatactgca gctttactgc cttcctcctt atcctacagt acaatcagca gtctagttct      540
tttcatttgg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc      600
atc                                          603

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<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

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<400> 12
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1          5          10          15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
          20          25          30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
          35          40          45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
          50          55          60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65          70          75          80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
          85          90          95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
          100          105          110

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Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
atgaagacac tccagttttt ctctcttttc tgttgctgga aagcaatctg ctgcaatagc 60
tgtgagctga ccaacatcac cattgcaata gagaaagaag aatgtcggtt ctgcataagc 120
atcaacacca cttgggtgtgc tggctactgc tacaccaggg atctgggtgta taaggaccca 180
gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggatatatga aacagtgaga 240
gtgccccggt gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtgt 300
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccagc 360
tactgctcct ttggtgaaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
 100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
 115 120 125

Glu

<210> 15
 <211> 1342
 <212> DNA
 <213> Homo sapiens

<400> 15
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 ccgccctctc ctccaggccc gtggggctgg ccctgcaccg ccgagcttcc cgggatgagg 120
 gcccccggtg tggtcacccg gcgcgcccga ggtcgctgag ggaccccggc caggcgcgga 180
 gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc 240
 totgggcctc ccagtcctgg gcgccccacc acgcctcctc tgtgacagcc gagtcctgga 300
 gaggtacctc ttggaggcca aggaggccga gaatatcaag acgggctgtg ctgaacactg 360
 cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag 420
 gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc 480
 tgtcctgcgg ggccaggccc tgttggtcaa ctcttcccag ccgtgggagc ccctgcagct 540
 gcatgtggat aaagccgtca gtggccttcg cagcctcacc actctgcttc gggctctgcg 600
 agcccagaag gaagccatct cccctccaga tgcggcctca gctgctccac tccgaacaat 660
 cactgctgac actttccgca aactcttcg agtctactcc aatttcctcc ggggaaagct 720
 gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccagggtg tgtccacctg 780
 ggcatatcca ccacctccct caccaacatt gcttgtgcca caccctccc cgccactcct 840
 gaaccccgtc gaggggctct cagctcagcg ccagcctgtc coatggacac tccagtgcc 900
 gcaatgacat ctcaggggccc agaggaactg tccagagagc aactctgaga tctaaggatg 960
 tcacagggcc aacttgaggg ccagagcag gaagcattca gagagcagct ttaaactcag 1020
 ggacagagcc atgctgggaa gacgcctgag ctactcggc accctgcaa atttgatgcc 1080
 aggacacgct ttggaggcga ttacctggt ttcgcaccta ccatcaggga caggatgacc 1140

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tggagaactt aggtggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt 1200
gggtggcaaga gcccccttga caccgggggtg gtgggaacca tgaagacagg atgggggctg 1260
gcctctgggt ctcatgggggt ccaagttttg tgtattcttc aacctcattg acaagaactg 1320
aaaccaccaa aaaaaaaaaa aa 1342

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<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

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<400> 16

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1           5           10           15

```

```

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
          20           25           30

```

```

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
          35           40           45

```

```

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50           55           60

```

```

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65           70           75           80

```

```

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
          85           90           95

```

```

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100           105           110

```

```

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115           120           125

```

```

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
130           135           140

```

```

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145           150           155           160

```

```

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu

```

165

170

175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 17
 atgtggctgc agagcctgct gctcttgggc actgtggcct gcagcatctc tgcacccgcc 60
 cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg 120
 cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac 180
 tcagaaatgt ttgacctcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240
 cagggcctgc ggggcagcct caccaagctc aagggcccct tgaccatgat ggccagccac 300
 tacaagcagc actgcctcc aaccccgaa acttctgtg caaccagat tatcacottt 360
 gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag 420
 ccagtccagg agtga 435

<210> 18
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

<210> 19
<211> 501
<212> DNA
<213> Homo sapiens

<400> 19
atgaaatata caagttatat cttggctttt cagctctgca tcgttttggg ttctcttggc 60
tgttactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca 120
ggtcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
gaggagagt acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt 240
aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300
aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360
tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420
gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
ggtcgaagag catcccagta a 501

<210> 20
<211> 166
<212> PRT
<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu

20	25	30
Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn		
35	40	45
Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp		
50	55	60
Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe		
65	70	75 80
Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile		
	85	90 95
Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg		
	100	105 110
Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val		
	115	120 125
Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser		
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Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg		
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Gly Arg Arg Ala Ser Gln		
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<210> 21
 <211> 1352
 <212> DNA
 <213> Homo sapiens

<400> 21
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<210> 22
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 22

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Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 20 25 30

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415

Gln Lys

<210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens

<400> 23
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<210> 24
 <211> 536
 <212> PRT

<213> Homo sapiens

<400> 24

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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
 20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
 65 70 75 80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu

[illegible]

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp His Arg Gln
 530 535

<210> 25
 <211> 1726
 <212> DNA
 <213> Homo sapiens

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 gagttctgca gcacccctgc ctgctctgag ggaaacagtg actgctactt tgggaatggg 660
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 tccatgatcc tgataggcaa ggtttacaca gcacagaacc ccagtgccca ggcactgggc 780

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gatgtcccg gtgtgtacac caaggttacc aactacctag actggattcg tgacaacatg     1680
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<210> 26
 <211> 562
 <212> PRT
 <213> Homo sapiens

<400> 26

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
          20           25           30

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Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35           40           45

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Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
50           55           60

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Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65 70 75 80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
85 90 95

Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
100 105 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
115 120 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
130 135 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
145 150 155 160

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
165 170 175

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
180 185 190

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
195 200 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
210 215 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
245 250 255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
260 265 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
275 280 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr

290	295	300
Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala		
305	310	315 320
Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro		
	325	330 335
Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile		
	340	345 350
Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu		
	355	360 365
Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu		
	370	375 380
Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp		
385	390	395 400
Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser		
	405	410 415
Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro		
	420	425 430
Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly		
	435	440 445
Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys		
	450	455 460
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His		
465	470	475 480
Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr		
	485	490 495
Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp		
	500	505 510
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val		
	515	520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
 530 535 540

Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560

Arg Pro

<210> 27
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 27
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<210> 28
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 28

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 <212> PRT
 <213> Homo sapiens

<400> 30

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          20           25           30

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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
          35           40           45

```

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Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
          50           55           60

```

```

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65           70           75           80

```

```

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
          85           90           95

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Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
 100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
 115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
 130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
 145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
 165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
 180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
 195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
 225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
 290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
 305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
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Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
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Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
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Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
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Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
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Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
 515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
 530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg

545	550	555	560
Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu			
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Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val			
	580	585	590
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu			
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	610	615	620
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val			
	625	630	635
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp			
	645	650	655
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe			
	660	665	670
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr			
	675	680	685
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro			
	690	695	700
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly			
	705	710	715
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp			
	725	730	735
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys			
	740	745	750
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg			
	755	760	765
Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp			
	770	775	780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
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Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
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Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
820 825 830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
835 840 845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
865 870 875 880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
885 890 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
900 905 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
915 920 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
930 935 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
945 950 955 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
965 970 975

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
980 985 990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
995 1000 1005

Leu Phe	Lys Val	Ser Ile	Ser	Leu Leu	Lys Thr	Asn	Lys Thr	Ser
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Asn Asn	Ser Ala	Thr Asn	Arg	Lys Thr	His Ile	Asp	Gly Pro	Ser
1025			1030			1035		
Leu Leu	Ile Glu	Asn Ser	Pro	Ser Val	Trp Gln	Asn	Ile Leu	Glu
1040			1045			1050		
Ser Asp	Thr Glu	Phe Lys	Lys	Val Thr	Pro Leu	Ile	His Asp	Arg
1055			1060			1065		
Met Leu	Met Asp	Lys Asn	Ala	Thr Ala	Leu Arg	Leu	Asn His	Met
1070			1075			1080		
Ser Asn	Lys Thr	Thr Ser	Ser	Lys Asn	Met Glu	Met	Val Gln	Gln
1085			1090			1095		
Lys Lys	Glu Gly	Pro Ile	Pro	Pro Asp	Ala Gln	Asn	Pro Asp	Met
1100			1105			1110		
Ser Phe	Phe Lys	Met Leu	Phe	Leu Pro	Glu Ser	Ala	Arg Trp	Ile
1115			1120			1125		
Gln Arg	Thr His	Gly Lys	Asn	Ser Leu	Asn Ser	Gly	Gln Gly	Pro
1130			1135			1140		
Ser Pro	Lys Gln	Leu Val	Ser	Leu Gly	Pro Glu	Lys	Ser Val	Glu
1145			1150			1155		
Gly Gln	Asn Phe	Leu Ser	Glu	Lys Asn	Lys Val	Val	Val Gly	Lys
1160			1165			1170		
Gly Glu	Phe Thr	Lys Asp	Val	Gly Leu	Lys Glu	Met	Val Phe	Pro
1175			1180			1185		
Ser Ser	Arg Asn	Leu Phe	Leu	Thr Asn	Leu Asp	Asn	Leu His	Glu
1190			1195			1200		
Asn Asn	Thr His	Asn Gln	Glu	Lys Lys	Ile Gln	Glu	Glu Ile	Glu
1205			1210			1215		

Lys	Lys	Glu	Thr	Leu	Ile	Gln	Glu	Asn	Val	Val	Leu	Pro	Gln	Ile
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His	Thr	Val	Thr	Gly	Thr	Lys	Asn	Phe	Met	Lys	Asn	Leu	Phe	Leu
1235						1240					1245			
Leu	Ser	Thr	Arg	Gln	Asn	Val	Glu	Gly	Ser	Tyr	Asp	Gly	Ala	Tyr
1250						1255					1260			
Ala	Pro	Val	Leu	Gln	Asp	Phe	Arg	Ser	Leu	Asn	Asp	Ser	Thr	Asn
1265						1270					1275			
Arg	Thr	Lys	Lys	His	Thr	Ala	His	Phe	Ser	Lys	Lys	Gly	Glu	Glu
1280						1285					1290			
Glu	Asn	Leu	Glu	Gly	Leu	Gly	Asn	Gln	Thr	Lys	Gln	Ile	Val	Glu
1295						1300					1305			
Lys	Tyr	Ala	Cys	Thr	Thr	Arg	Ile	Ser	Pro	Asn	Thr	Ser	Gln	Gln
1310						1315					1320			
Asn	Phe	Val	Thr	Gln	Arg	Ser	Lys	Arg	Ala	Leu	Lys	Gln	Phe	Arg
1325						1330					1335			
Leu	Pro	Leu	Glu	Glu	Thr	Glu	Leu	Glu	Lys	Arg	Ile	Ile	Val	Asp
1340						1345					1350			
Asp	Thr	Ser	Thr	Gln	Trp	Ser	Lys	Asn	Met	Lys	His	Leu	Thr	Pro
1355						1360					1365			
Ser	Thr	Leu	Thr	Gln	Ile	Asp	Tyr	Asn	Glu	Lys	Glu	Lys	Gly	Ala
1370						1375					1380			
Ile	Thr	Gln	Ser	Pro	Leu	Ser	Asp	Cys	Leu	Thr	Arg	Ser	His	Ser
1385						1390					1395			
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1400						1405					1410			
Ser	Phe	Pro	Ser	Ile	Arg	Pro	Ile	Tyr	Leu	Thr	Arg	Val	Leu	Phe
1415						1420					1425			
Gln	Asp	Asn	Ser	Ser	His	Leu	Pro	Ala	Ala	Ser	Tyr	Arg	Lys	Lys

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Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp 1490 1495 1500		
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His 1505 1510 1515		
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser 1520 1525 1530		
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Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser 1565 1570 1575		
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln 1580 1585 1590		
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Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys 1610 1615 1620		
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys 1625 1630 1635		
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg 1640 1645 1650		

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Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile	1685	1690	1695
Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys	1700	1705	1710
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr	1715	1720	1725
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Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr	1745	1750	1755
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His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp	1775	1780	1785
Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser	1790	1795	1800
Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly	1805	1810	1815
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Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu	1835	1840	1845
Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu	1850	1855	1860

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1880						1885					1890			
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1895						1900					1905			
Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn
1910						1915					1920			
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1925						1930					1935			
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Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser
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Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile
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Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn
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Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile
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Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg
2165						2170					2175			
Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	Asn	Ser	Cys
2180						2185					2190			
Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	Ala	Gln
2195						2200					2205			
Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	Trp	Ser
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Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn	Ala	Trp
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Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe
2240						2245					2250			
Gln	Lys	Thr	Met	Lys	Val	Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys
2255						2260					2265			
Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser
2270						2275					2280			
Ser	Gln	Asp	Gly	His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys

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<210> 31
<211> 1471
<212> DNA
<213> Homo sapiens
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<400>	31	
atggcgcccc	tgcgcgtctg	ggccgcgctg gccgtcggac tggagctctg ggctgccccg 60
cacgccttgc	ccgcccaggt	ggcatttaca ccctacgccc cggagccccg gagcacatgc 120
cggctcagag	aatactatga	ccagacagct cagatgtgct gcagcaaattg ctgcgcgggc 180
caacatgcaa	aagtcttctg	taccaagacc toggacacog tgtgtgactc ctgtgaggac 240
agcacatata	cccagctctg	gaactggggt cccgagtgct tgagctgtgg ctcccgtgt 300
agctctgacc	aggtggaaac	tcaagcctgc actcgggaac agaaccgcat ctgcacctgc 360
aggccccggt	ggtactgcgc	gctgagcaag caggaggggt gccggctgtg cgcgcgcgtg 420
cgcaagtgcc	gcccgggctt	cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg 480
tgcaagccct	gtgccccggg	gacgtttctc aacacgactt catccacgga tattttgcagg 540
ccccaccaga	tctgtaacgt	ggtggccatc cctgggaatg caagcatgga tgcagtctgc 600
acgtccacgt	ccccccaccg	gagtatggcc ccaggggcag tacacttacc ccagccagtg 660
tccacacgat	cccaacacac	gcagccaact ccagaaccca gcactgctcc aagcacctcc 720
ttcctgctcc	caatgggccc	cagcccccca gctgaaggga gcactggcga cttcgctctt 780
ccagttggac	tgatttgtgg	tgtgacagcc ttgggtctac taataatagg agtgggtgaac 840
tgtgtcatca	tgaccaggt	gaaaaagaag cccttgtgcc tgcagagaga agccaagggt 900
cctcacttgc	ctgccgataa	ggccccgggt acacagggcc ccgagcagca gcacctgctg 960

```

atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga 1020
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ggccggggcca gcaccgggag ctccagattct tcccctgggtg gccatgggac ccagggtcaat 1140
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agttaaccag gccggtgtgg gctgtgtcgt agccaagggtg ggctgagccc tggcaggatg 1440
accctgcgaa ggggccctgg tccttcagg c 1471

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<210> 32
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 32

```

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1           5           10           15

```

```

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
          20           25           30

```

```

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
          35           40           45

```

```

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50           55           60

```

```

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65           70           75           80

```

```

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
          85           90           95

```

```

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
          100          105          110

```

```

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
          115          120          125

```

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
 435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
 450 455 460

<210> 33
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 33
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 tcgtgagcga ctccaaaggc agcaatgaac ttcattcaagt tccatcgaac tgtgactgtc 180
 taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc 240
 caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300
 atggtcactt ttaccgagga aaggccagca ctgacaccat gggccggccc tgccctgccct 360
 ggaactctgc cactgtcctt cagcaaactg accatgccca cagatctgat gctcttcagc 420
 tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctggtgct 480
 atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcac ggtgcatgac tgcgcagatg 540
 gaaaaaagcc ctctctctct ccagaagaat taaaatttca gtgtggccaa aagactctga 600
 ggccccgctt taagattatt gggggagaat tcaccacccat cgagaaccag ccctgggttg 660
 cggccatcta caggaggcac cggggggggt ctgtcaccta cgtgtgtgga ggcagcctca 720

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tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattaccca aagaaggagg      780
actacatcgt ctacctgggt cgctcaaggc ttaactccaa cacgcaaggg gagatgaagt      840
ttgaggtgga aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca      900
acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgag ccatcccga      960
ctatacagac catctgcctg cctcgatgt ataacgatcc ccagtttggc acaagctgtg     1020
agatcactgg ctttggaata gagaattcta ccgactatct ctatccggag cagctgaaga     1080
tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg     1140
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gagactcagg gggaccctc gtctgttccc tccaaggcgc catgactttg actggaattg     1260
tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac     1320
acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg     1380
ccccagggag gaaacgggca ccaccgctt tcttgctggt tgtcattttt gcagtagagt     1440
catctccatc agctgtaaga agagactggg aagat                                  1475

```

```

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

```

```

<400> 34

```

```

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1           5           10           15

```

```

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
           20           25           30

```

```

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
           35           40           45

```

```

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
           50           55           60

```

```

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65           70           75           80

```

```

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
           85           90           95

```


Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
 180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
 195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
 210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
 225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
 245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
 260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 36
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 106
 <212> PRT
 <213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39
 <211> 1039
 <212> DNA
 <213> Homo sapiens

<400> 39
 tctctgcacag gcagtgcctt gaagtgcttc ttcagagacc tttcttcata gactactttt 60
 tttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120
 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg 180
 ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgcagcc 240
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300
 gtgcagatcc tgagccgcta tgacatgcc ctggtccagg aggtcagaga cagccacctg 360
 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480
 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgoga gccctgcggg 540
 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc 600
 agggagtttg ccattgttcc cctgcatgcg gcccggggg acgcagtagc cgagatcgac 660
 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg 720
 atgggcgact tcaatgcggg ctgcagctat gtgagacctt ccagtggtc atccatccgc 780
 ctgtggacaa gcccacctt ccagtggtg atccccgaca gcgctgacac cacagctaca 840
 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcggtt 900
 gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg 960
 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc 1020
 cacaccagtt gaactgcag 1039

<210> 40
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu

1	5	10	15
Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr	20	25	30
Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val	35	40	45
Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp	50	55	60
Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp	65	70	75
Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn	85	90	95
Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser	100	105	110
Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn	115	120	125
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe	130	135	140
Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly	145	150	155
Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val	165	170	175
Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn	180	185	190
Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu	195	200	205
Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr	210	215	220
Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly	225	230	235
			240

20	25	30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile 35 40 45		
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly 50 55 60		
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser 65 70 75 80		
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe 85 90 95		
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu 100 105 110		
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser 115 120 125		
Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val 130 135 140		
Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser 145 150 155 160		
Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg 165 170 175		
Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met 180 185 190		
Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn 195 200 205		
Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr 210 215 220		
Val Ser 225		
<210> 43		
<211> 450		

<212> DNA

<213> Homo sapiens

<400> 43

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gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc      60
gcctcctgcc cctgctggcg ctgctggccc tctggggacc tgaccagcc gcagcctttg      120
tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac      180
gaggcttctt ctacacaccc aagaccgcc gggaggcaga ggacctgcag gtggggcagg      240
tggagctggg cggggggcct ggtgcaggca gcctgcagcc cttggccctg gaggggtccc      300
tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg      360
agaactactg caactagacg cagcccgagc gcagccccc acccgccgcc tctgcacccg      420
agagagatgg aataaagccc ttgaaccagc      450

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<210> 44

<211> 110

<212> PRT

<213> Homo sapiens

<400> 44

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Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1           5           10           15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
          20           25           30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
          35           40           45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
          50           55           60

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65           70           75           80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
          85           90           95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
          100          105          110

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<210> 45

<211> 1203
 <212> DNA
 <213> Hepatitis B virus

<400> 45
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 cctctgggat tctttcccgga tcaccagttg gacctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180
 ggagacttcg ggccagggtt caccacacca caggcggtc ttttggggtg gagccctcag 240
 gctcagggca tattgacaac agtgccagca ggcctcctc ctgtttccac caatcggcag 300
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcatcc tcaggccatg 360
 cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagttag gggcctatat 420
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 atatogtcaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca 540
 ggattcctag gacctctgct cgtgttacag gcgggggttt tcttggtgac aagaatcctc 600
 acaataccac agagtctaga ctctgggtg acttctctca attttctagg gggagcacc 660
 acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccaac ctcttgcct 720
 ccaatttgct ctggttatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 780
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 cctgctcaag gaacctctat gtttccctct tgttgctgta caaaaccttc ggacggaaac 960
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 tga 1203

<210> 46
 <211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 385 390 395 400

<210> 47
 <211> 799
 <212> DNA
 <213> Homo sapiens

<400> 47
 cgaaccactc agggctctgt ggacagctca cctagctgca atggctacag gctcccgga 60
 gtcctgtctc ctggcttttg gctgtctctg cctgccctgg cttcaagagg gcagtgcctt 120
 cccaaccatt cccttatcca ggccttttga caacgctatg ctccgcgccc atcgtctgca 180
 ccagctggcc tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa 240
 gtattcatto ctgcagaacc ccagacctc cctctgtttc tcagagtcta ttccgacacc 300

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ctccaacagg gaggaacac aacagaaatc caacctagag ctgctccgca tctccctgct 360
gctcatccag tcgtggctgg agcccgtgca gttcctcagg agtgtcttcg ccaacagcct 420
ggtgtacggc gcctctgaca gcaacgtcta tgacctccta aaggacctag aggaaggcat 480
ccaaacgctg atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca 540
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<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

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<400> 48

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Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
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Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
          20           25           30

```

```

Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
          35           40           45

```

```

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
          50           55           60

```

```

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
          65           70           75           80

```

```

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
          85           90           95

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Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
          100          105          110

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Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
          115          120          125

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Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
 130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
 145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
 165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
 180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
 195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

<210> 49
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 49
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<210> 50
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
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Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
 20 25 30

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
 35 40 45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
 50 55 60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
 65 70 75 80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
 85 90 95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120 125

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 100 105

<210> 52
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 52

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
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Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 53
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 53

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 54

<211> 119

<212> PRT

<213> Mus musculus

<400> 54

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr
 1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
 100 105 110

Thr Leu Val Thr Val Ser Ala
 115

<210> 55
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 55

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 56
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 56

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

340

345

350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

<210> 57
 <211> 8540
 <212> DNA
 <213> Homo sapiens

<400> 57
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